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	868-60-sn	sión 5.1.6 003 Compügen Ltd.	lel. Search time 73 seconds (wathout alignments) 1122.591 Million cell updates/sec	ii ii Mapkawi			imeters: 61	90	A_Geneseq_101002:*	predicted by chance to have a score of the result being printed, otal score distribution.	RIES Description	Novel human secret Human transferase Peptide #7772 enco Protein #6682 enco Human brain expres Human bone marrow Peptide #7984 enco Human peptide enco Human ovarian anti Human disease rela
ر مُفتحد	Jun 5 08:31:25 2003	GenCore version Copyright (c) 1993 - 2003	- protein search, using sw mod May 30, 2003, 12:20:35	US-09-898-165B-7 score: 615 : MSGIKKQKTENQQKSTNVVY		10	of hits satisfying chosen p eq length: 0 eq length: 2000000000	Post-processing: Listing first 1000 summaries		o. is the number of results reater than or equal to the derived by analysis of the t	SUMMARIES QUETY Score Match Length DB ID	288 46.8 648 22 AAU324.38 221 35.9 619 21 AAY79214 65 10.6 65 22 ABB40266 65 10.6 65 22 AAB61026 65 10.6 65 22 AAM61056 65 10.6 65 22 AAM73760 65 10.6 65 22 AAM73760 65 10.6 65 23 AAM73760 65 10.6 65 23 AAM73760 85 10.6 65 23 AAM73760 86 10.6 65 23 AAM73760 87 AAM73760 88 133 23 ABG41780 38 6.2 624 19 AAW70494
<u> </u>	Thu J		OM protein Run on:	Title: Perfect sc Sequence:	Scoring table	Word size	Total number Minimum DB se Maximum DB se	Post-proce	Database	Pred. N score g and is	Result No. 8	10843351

Human apps kinase/A
Human secreted pro
Fragment of human
Arabidopsis thalia
Bedenfichia coli p
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Scokean Adenylylsulph ene therapy; nutritional supplement; on; haematopoiesis; nerve tissue regeneration; mmune stimulation; anti-inflammatory; leukaemia ALIGNMENTS protein #2929 Ş tein; 648 ntry)  $\frac{1}{2}$ Homo sapiens. XX OS NA PN

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gastrointestinal disorder; developmental disorder; genetic disorder; neurological disorder; reproductive disorder; smooth muscle disorder; immunological disorder; inflammation; diagnosis; therapy; ATP sulfurylase/APS kinase 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to
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                                                                                                                                                                                                                                                                                                        polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for
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                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF
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                                                                                                                                                    Liu C, Drmanac RT;
                                           16-APR-2001; 2001WO-US08656
                                                                        18-APR-2000; 2000US-0552929 26-JAN-2001; 2001US-0770160
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nes 288; Conserv
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treating cancers and developmental, gastrointestinal, genetic, immunological, neurological, reproductive and smooth muscle disorders
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Location/Qualifiers
92
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                                                                                        "potential
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308
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N-PSDB; AAZ94206.
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Hillman JL,
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AAY79214 standard; Protein; 619 AA.

Human transferase TRNSFS-6

19-JUN-2000

S S S E S E S

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                              Claim 27; SEQ ID NO 32901; 639pp + sequence listing; English.
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2000US-0207456.
2000US-0608408.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Matches 65; Conservative
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30-JUN-2000;
03-AUG-2000;
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"TRNSFS-6 is expressed in cardiovascular, gastrointestinal, reproductive and endocrine cardiovascular, gastrointestinal, reproductive and endocrine cardiovascular, gastrointestinal, reproductive and endocrine can be used in the diagnosis, prevention and treatment of cancer, can be used in the diagnosis, prevention and treatment of cancer, concerned by the diagnosis, prevention and treatment of cancer, concerned disorders, gastrointestinal disorders, genetic disorders, immunological disorders, reproductive disorders, and smooth muscle disorders. The complete concerned to raise antibodies, and to screen considerate and antagonists of transferate activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                    35.9%; Score 221; DB 21; thength 619; 99.7%; Pred No. 13.7e=214; trive 0; Mismatches 1; Inder-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #7772 encoded by human foetal liver single exon probe.
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26-MAY-2000; 2000US-0207456.
30-UNN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236399.
04-OCT-2000; 2000GB-0024263.
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Matches 321; Conservative
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                                                                                                                                               Protein #6682 encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
10.6%; Score 65; DB 22; Length 65; 100.0%; Pred. No. 2.1e-57; tive 0; Mismatches 0; Indels
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of nervous system

treatment

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The present invention relates to single exon nucleic acid propes for measuring human gene expression in a sample derived firsh human heart (see ABA21355-ABA41305). The present sequence is a protein encoded, by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing adding, staging, monitoring and prognessing diseases of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained. No electronic format directly from WIPO at the wipo int/pub/published_pit_sequences.
                                                                                                                                                                                                                                                                                BEYLVSHAIPCYSLDGDNVRHGLNRNIGFSPGDREENIRRIAEVAKLFADAGLVCITSFI 122
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                            Local Similarity
les 65; Conserv
                                                                                                                                                                                                                                                                                                                                              SPFAK 127
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                                                                                                                                                                                                                                                                                                                                                                    SPFAK 65
                                                                                                                                                                                                    65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM61056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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                                                                                                                            63 EEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFI 122
                  cancers. The present sequence is a protein encoded by one of the invention.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 34066; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                              Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                            probe encoded protein SEQ
                                                                              Score 65; DB 22; I
Pred, No. 2.1e-57;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; L
2.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
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                                                                      10.6%; Scur
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%; Sco.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
which may enable the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                       AAM73760 standard; Protein;
                                                                                                                                                                                                                                                                                                                             expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000GB-0024263
                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100.
Matches 65, Conservative
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53
                                                                                          Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                         SPFAK 127
                                                                                                                                                                                                                                                                                                                          bone marrow
                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                  the probes
                                                                                                                                                                         123
                       epilepsy
                                                         Sequence
                                                                               Query Match
                                                                                                                                                                                                                                                                              AAM73760;
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                                                                                                                                                                                                                                                                                                                            Human
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single, exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising qa conlection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene comprising of the exons in the issues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene carposopen reading frames (ORF). The probes are used for gene carposopen reading frames (ORF). The probes are used for gene carposopen reading frames (ORF). The probes are used for gene carposopen reading frames (ORF). The study of lung diseases corpusable manalysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 33309; 634pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                Peptide #7984 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 65;
                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 65; DB 22; Length 65
100.0%; Pred. No. 2.1e-57;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 34216; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                 AAM33947 standard; Protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359.
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                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 65; Conservative
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                                                           SPFAK 127
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SPFAK 65
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                                                                                                                                                                                                                                                                                                          genetic disorder
                                                                                                                                                                                                                                                                                                                                                                      WO200157272-A2.
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03-AUG-2000;
21-SEP-2000;
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04-OCT-2000;
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                              Н
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63
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                                                                                                                                      RESULT 7
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RESULT 8 ABG43644

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Human peptide encoded by genome-derived single exon probe SEQ ID 33309.
                                                                                                                                                                                                                                                                                                                                                 Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioledenomyoncosis; Karagener syndrome; pulmonary alveolar proteinnosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                                                                                                                                               interstitial lung disease;
                                                                                                                                                                                                                              Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung dise familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; daucher's disease; Niemann-bick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
ABG43644 standard; Peptide; 65 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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2000US-234687P.
2000US-236359P.
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2000US-0608408.
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                                                                                                             19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114183/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                         ABG43644;
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ABP41780;
ABP41780;
T 22-AUG-2002 (first entry)
XX
KW
Human ovarian antigen HMEJA45, SEQ, ip No. 2912
XX
KW
Human; ovarian antigen; ovary; ovarian; breat; cancer; tumour; veproductive system disorder; ovarian cancer; tumour; reproductive system disorder;
XW
My infertility; pregnancy disorder: adovidation; polycystic ovary syndrome; pcOS; ovarian capt; dysmeorrhoea; endocrine disorder;
XW
My infertility; pregnancy disorder: adovidation; polycystic ovary syndrome;
XW
My ardiovascular disorder; respiratory disorder; drug screening;
XW
My astrointestinal disorder; urinary system disorder; drug screening;
XW
My antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XW
My antihody preparation; cytostatic; immunomodulatory; neuroprotective;
XW
My antihody preparation; reproductive.
                                                                                                                                                                                                                                                                                                                         63 EEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFI 122
                                                                                                                                                                                                                                                                                                                                          (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosidenosis, pulmonary histocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hypline membrane disease. The present sequence is, a peptide/protein note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                    10.6%; Score 65; DB 23; Length 65; 100.0%; Pred. No. 2.1e-57; Live 0; Mismatches 0; Indels
                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                         Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-147878/19.
N-PSDB; ABQ54857.
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                                                                                                                                                                                                                          65 AA;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polypuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen so polypuclectides, antibodies against human ovarian antigens, and the use of ovarian polypuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and metastratic tumnours of ovarian or breast origin, reproductive system of isorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HTV, toxoplasanosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired the conformed infections antolmmune oophoritis, systemic lupus erythematosus), cardiovascular disorders, inclammatories, autoimmune oophoritis, systemic lupus erythematosus), crespiratory disorders (e.g., anaemia), cardiovascular disorders and uninary system disorders. Ovarian antigen polypeptides and conditions (e.g., anaemia), cardiovascular disorders and uninary system disorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies used unan ovarian antigen of the invention. The present consequence represents a human ovarian antigen of the invention of the present of the pritient of the sequence data for this patent did oot form part of the printed specification, but was obtained in electronic format directly from WIPO certification, but was obtained in electronic format directly from WIPO certification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human disease related nucleotide kinase-2; DRNK-2; deoxyguanosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human disease related nucleotide kinase-2 (DRNK-2) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "adenosine 3'-phosphate 5'-phosphosulfate (PAPS)-dependent enzyme motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p21ras; cell proliferation; oncogenesis; cancer; PAPS; inmune disorder; neurological dysfunction; gene therapy; adenosine 3'-phosphate 5'-phosphosulfate-dependent enzyme motif; ATP pyrophosphatase PP-motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.9%; Score 55; DB 23; Length 133; Best Local Similarity 100.0%; Pred. No. 5.1e-47; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59..66
/note= "ATP/GTP binding site (p-loop)"
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/note= "ATP pyrophosphatase PP-motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylated"
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified·site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW70494;
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AAW70494
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US5817482-A.

Claim 11; SEQ ID No 2912; 2922pp; English.

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97US-0048154
97US-0048160
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                                                                                                                                                                                                                                                                                                   Query Match 6.2°
Best Local Similarity 100.
Matches 38; Conservative
              (NIRA ) UNITIKA LTD.
(HUMA-) ZH HUMAN SCI
                                                          WPI; 1999-451549/38.
N-PSDB; AAX84897.
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                                                                                                                                                                                                                                                                     624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW67882;
                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                         As The present sequence represents a human disease related nucleotide
kinase-2 (DRNK-2) protein sequence: The DNKR-2 encoding DNA sequence
consists identified in Incyte Clone 37887 from the lung tissue cDNA
consists identified in Incyte Clone 37887 from the lung tissue cDNA
consists identified in Incyte Clone 37887 from the lung tissue cDNA
consists in Incyte Clone 37887 from the lung tissue cDNA
consists now far may may are deoxyganosine kinases, which catalyse
consists now far probably are deoxyganosine kinases, which catalyse
consists of a terminal phosphate from adenosine triphosphate (ATP)
consists of a terminal phosphate from adenosine triphosphate.
Consists of CGTP and its corresponding nucleoside triphosphate.
Consists are known to control the activity of certain oncogenic
concogenesis, suppression of the enzyme activity causes high ratios of
concogenesis, suppression of the enzyme activity causes high ratios of
concogenesis, suppression of the enzyme activity causes high ratios of
concogenesis, suppression of treated with the recombinant enzyme, or by
concogened strategies. Anti-sense constructs of the DNKR
concogened strategies and be used for inhibition of over-expression
                                                                                                                                                                                                                                       caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                   Nucleic acids encoding de:oxy:guanosine kinase - useful for recombinant production of the enzyme for treating diseases callack of the enzyme e.g. cancers caused through loss of enzyme
                                                                                                                                        Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                                                                                        Guegler KJ; . Hawkins .PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 38; DB 19;
100.0%; Pred. No. 3e-29;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human APS kinase/ATP sulphurylase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APS kinase/ATP sulphurylase; human; PAPS
                                                                                                                                                                                                                                                                                         Examples; Fig 2A-2G; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3'-phosphoadenosine 5'-phosphosulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY22349 standard; Protein; 624 AA.
                                                                          97US-0879561
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                                            97US-0879561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%
Best Local Similarity 100.(
Matches 38; Conservative
                                                                                                        (INCY-) INCYTE PHARM INC.
                                                                                                                                        Corley NC,
                                                                                                                                                                    WPI; 1998-556388/47.
N-PSDB; AAV33482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 AA;
                                            20-JUN-1997;
                                                                          20-JUN-1997;
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             06-OCT-1998
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                                                                                                                                                                                                                                                                     Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                           This sequence is the human-derived APS kinase/ATP.sulphurylase of the invention. The enzyme may be used to prepare 3'-phosphoadenosine 5'-phosphosulphate (PAPS) on a large scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                     New human-derived APS kinase/ATP sulfurylase gene - useful for
large scale preparation of 3'-phosphoadenosine 5'-phosphosulfate
(PAPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 38; DB 20; Length 624; 100.0%; Pred. No. 3e-29; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein encoded by gene 76 clone HOSFD58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
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SHINKO ZAIDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW67882 standard; Protein; 625 AA.
                                                                                                                                                                                                                                                                                                              Claim 1; Page 6-7; 9pp; Japanese.
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970S-004033.
970S-0040334.
970S-0040336.
970S-0040311.
970S-0043311.
970S-0043313.
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97US-0043568.
97US-0043569.
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97US-0048964
97US-0048974
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97us-00519
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97US-0047
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                                                                                                                                                                                                                                                                                          11-APR-1997
                                                                                                                                                                                                                                  11-APR-1
                                                                                                                                                                                                                                                                                                                                     This sequence represents a secreted human protein encoded by the generate clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immosplobilin FC portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 8 novel genes and their fragments (nucleic red sequences: AAX00611-X00724; amino acid sequences AAX06041)

Which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the presence of mutations in polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses)
                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 38; DB 20; Length 625; larity 100.0%; Pred. No. 3e-29; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                           Retrie AM, Florence KA:
DW, Moore PA, Ni, J', Olsen HS;
Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; testis; tumour; foetal brain tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                       Lafleur DW
                                                                                                                                                            Ebner R,
                                        970S-0048350.
970S-0048351.
970S-0048352.
970S-0048355.
970S-0054804.
 97US-0048186.
97US-0048187.
97US-0048188.
                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                         Brewer LA, Duan R,
Greene JM, Hu JS, L
Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 38; Conservat
                                                                                                                                                                                                                WPI; 1999-070066/06.
N-PSDB; AAX00686.
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
05-AUG-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                              Arabidopsis thaliana protein fragment SEQ ID NO: 55117.
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99US-0139463.
99US-0139750.
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99US-0123548
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99US-0134219
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99US-0138847
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   This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule designated Gene 14 (AAV59524).

The gene can be used to generate fusion proteins by linking to the gene to a buman immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74711-W75026) which are useful for preventing, freating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Rosen CA;
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Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 36; Conservative 0; Mismatches 0;
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her CL, Florence KA,
Y, Moore PA, Ni J,
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Soppet DR,
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Lafleur DW,
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Ruben SM,

Feng P, Kyaw H,

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AAG44041;

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RESULT 14 AAG44041

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Sequence

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Length 373;

Score 22; DB 21; Pred. No. 2.8e-13; Mismatches 0;

AA.

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99US-0143624.
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Arabidopsis thaliana
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99US-0161992.
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Length 460; 0; 'Indels Query Match 3.6%; Score 22; DB 21; Best Local Similarity 100.0%; Pred. No. 3.4e-13 Matches 22; Conservative 0; Mismatches C

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Search completed: May 30, 2003, 12:30:13 Job time: 75 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:

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Title: Perfect score: Sequence:

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262574 seqs, 29422922 residues Searched:

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Database :

Issued\_Patents\_AA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 635, App	Sequence 3, Appli	Sequence 9, Appli	Sequence 634, App	Sequence 10, Appl	Sequence 2, Appli	Sequence 11, Appl	. ,	Sequence 6, Appli	10,	Sequence 8, Appli		Sequence 637, App	Sequence 4517, Ap
	ID	US-09-149-476-635	US-08-879-561-3	US-08-879-561-9:	US-09-149-476-634	US-09-346-408-10	US-09-346-408-2	US-09-346-408-11	US-09-346-408-4	US-09-346-408-6	US-08-879-561-10	US-09-346-408-8	US-09-346-408-12	US-09-149-476-637	US-09-134-001C-4517
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## ALIGNMENTS

		9149476			-	Secreted proteins	
		O/SD c				Human	
RESULT 1	US-09-149-476-635	; Sequence 635, Application US/09149476	; Patent No. 6420526	; GENERAL INFORMATION:	; APPLICANT: Rosen et al.	; TITLE OF INVENTION: 186 Human Secreted proteins	; FILE REFERENCE: PZ002P1

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9/149 US98/ 40,16 40,33 38,62 40,62	040,336 040,163 047,600 047,600 047,502 047,583 047,583 047,583 047,584 047,584 047,584 047,587	047,612 047,632 047,601 043,580 043,568 043,314 043,569
ER: US/ 3-09-08 3-03-06 3-03-06 3-03-06 5-03-07 5-03-07 5-03-07 5-03-07	ER: 60/ 7-63-60/ 7-63-60/ 7-63-60/ 7-63-60/ 7-63-60/ 8-60/	97.05-23 98-8:60/ 97.05-62/ 97.05-62/ 97.05-23/ 97.05-23/ 97.04-11/ 97.04-11/ 97.04-11/ 97.04-11/ 97.04-11/ 97.04-11/
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APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
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PPLICATION NUMBER: 60/043,315
LING DATE: 1997-04-11
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ILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,845
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ICATION NUMBER: 60/056,882
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PPLICATION NUMBER: 60/056,910
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FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                      ICATION NUMBER: 60/056,886
                                                                                                                                                                                                                                                                      PPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                                                                                                                     LICATION NUMBER: 60/056,878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICATION NUMBER: 60/056,872
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                                                                                                                                                                                                                                                                                                                                                                                   ICATION NUMBER: 60/056,630
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NG DATE: 1997-08-22
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ING DATE: 1997-08-22
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1997-04-1
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
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TLING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,875
TLING DATE: 1997-08-22
ILING DATE: 1997-05-23

PPLICATION NUMBER: 60/047,594

ILING DATE: 1997-05-23

PPLICATION NUMBER: 60/047,589

ILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                     PPLICATION NUMBER: 60/047,593
ILING DATE: 1997-05-23
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PPLICATION NUMBER: 60/043,576
ILING DATE: 1997-04-11
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LING DATE: 1997-08-22
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ILING DATE: 1997-08-22
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LING DATE: 1997-08-22
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TILING DATE: 1997-08-22
PPLICATION NUMBER: 60/048,964
ILING DATE: 1997-06-06
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LING DATE: 1997-09-05
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                                                                                                                        PPLICATION NUMBER: 60/047,614
                                                                                                                                                          APPLICATION NUMBER: 60/043,578
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Guegler, Karl J.
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Best Local Similarity 100.
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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APPLICANT: Bandma
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APPLICANT:
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                    EARLIER
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Length 624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
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EARLIER FILLIG DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER FILLIG DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILLING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/047,617
EARLIER APPLICATION NUMBER: 50.047,617
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,633
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EARLIER APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 634, Application US/09149476 Patent No. 6420526
                    FILING DATE:
ATTORNEY/AGENE INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-05-23
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                                                                                                                                                                                                                                                            LENGTH: 624 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                        ; LIBRARY: GenBank
; CLONE: 1109676
US-08-879-561-9
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Best Local Similarity
Matches 38; Conserv
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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Pred. No. 8e-29;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
                                                                                                                                                                          SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   US/08/879,561
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Patent No. 5817482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.2%; Sco
Best Local Similarity 100.0%; Pi
Matches 38; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET UNMBER: PR-
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 624 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                   Herewith
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     APPLICATION NUMBER:
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CLONE: 373887
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STATE: CA
Palo Alto
                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                           USA
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US-08-879-561-3
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                                           COUNTRY:
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1997-05-23 NUMBER: 60/047,592 1997-05-23 NUMBER: 60/047,581 1997-05-23 1997-05-23 NUMBER: 60/047,500 1997-05-23 1997-05-23 NUMBER: 60/047,500 1997-05-23 NUMBER: 60/047,590 NUMBER: 60/047,598	1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-04-11	60/043, 6 60/043, 6 4-11 4-11 60/043, 3 60/043, 3 4-11 4-11 4-11 60/056, 8 8-22 60/056, 8 8-22 8-
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R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,888

R APPLICATION NUMBER: 60/056,879

R TILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,899

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,880

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056, 894
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 636
APPLICATION NUMBER: 60/056, 874
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 814
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 814
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 810
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056, 864 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,586
ILING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,590
ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,595 ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,599 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22 ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/057,761
ILING DATE: 1997-08-22 ING DATE: 1997-05-23 LICATION NUMBER: 60/047,588 ING DATE: 1997-05-23 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,585 ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,589 TLING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,593 TILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-05-23 ILING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,875 ILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 APPLICATION NUMBER: 60/047,594 PPLICATION NUMBER: 60/047,614 ILLING DATE: 1997-05-23 PPLICATION NUMBER: 60/043,578 APPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/056,876 LICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,909 1997-08-22 1997-08-22 997-05-2 LING DATE: 1997-04-1 EARLIER
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US-09-346-408-11
S-09-346-408-11
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S-09
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APPLICANT: Anderson, Shawn
APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
CURRENT REPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER APPLICATION NUMBER: 11 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%; Score 22; DB 4; Length 465; 100.0%; Pred. No. 2.9e-13; Live 0; Mismatches 0; Indels
                                                                                                                                                                 Length 133;
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Pred. No. 9.8e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/346,408B CURRENT FILING DATE: 1999-07-01 EARLIER APPLICATION NUMBER: 60/092,833 , BARLIER FILING DATE: July 14, 1998 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 NADAVFAFQLRNPVHNGHALLM 260
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                                                                                                                                                                 Query Match 3.6%; Sc.
Best Local Similarity 100.0%; P.
Matches 22; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Solanum tuberosum
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Best Local Similarity 100.0
Matches 22; Conservative
                                   ; TYPE: PRT; ORGANISM: Zea mays US-09-346-408-2
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US-09-346-408-4
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LENGTH: 133
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
TITLE OF INVENTION GENES ENCODING SULFARENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FLING DATE: July 14, 1998
NUMBER OF SEO ID NOS: 12
SOFTWARE: Microsoft Office 97
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TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
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6.3e-28;
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CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 36; Best Local Similarity 100.0%; Pred. No. Matches 36; Conservative 0; Mismatcl
                                                     FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/057,650
                                                                                                                          EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                   60/048,964
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GENERAL INFORMATION:
FILING DATE: 1997-08-22
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                            ION NUMBER:
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
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APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Reference and Carl
APPLICANT: Reference and Canaba
FILE NEFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
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TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
                                                                                                                                                                                                                                                                                       Length 610;
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100.0%; Pred. No. 3.6e-13;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
SOFTWARE: MICROSOFT OF STATE OF THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                    401 NADAVFAFQLRNPVHNGHALLM 422
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09346408B Patent No. 6338966
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    415-855-0555
415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                      LENGTH: 610 amino acids
                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.45
Best Local Similarity 100.0
Matches 21; Conservative
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                   linear
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TOPOLOGY: Illec.
IMMEDIATE SOURCE:
LIBRARY: GenBan
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      TELEPHONE:
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Best Local Sim:
Matches 22;
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER PILING DATE: 1999-07-01
EARLIER FILING DATE: July 14, 1998
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CORRESPONDENCE ADDRESS:
ADDRESSFR
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FastSEQ for Windows Version 2.0
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TOWNERS: PF-0325 US
  NADAVFAFQLRNPVHNGHALLM 422
                         241 NADAVFAFQLRNPVHNGHALLM 262
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FILING DATE: Herewith
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                                                                                                                                        Sequence 6, Application US/09346408B Patent No. 6338966
GENERAL INFORMATION:
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Patent No. 5817482
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM COMPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Glycine max US-09-346-408-6
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PPLICATION NUMBER: 60/047,582 ILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,601
APPLICATION NUMBER: 1997-05-23
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
                                                                                                     APPLICATION NUMBER: 60/047,612
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NG DATE: 1997-04-11
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,880
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APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
                                                                                                                                                                                                                      APPLICATION NUMBER: 60/043,580
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER:
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ches 0;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                             Query Match 3.4%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 21; Conservative 0; Mismatches
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APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,581
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                                                                                                                                                                          402 ADAVFAFQLRNPVHNGHALLM 422
                                                                                                                                                                                                                                                                                                           Sequence 637, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-09-346-408-12
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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US-09-149-476-637
LENGTH: 476
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ő ΩD APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

Sequence 4517, Application US/09134001C Patent No. 6380370

-09-134-001C-4517

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4517

; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4517

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APPLICATION NUMBER: 60/047,595 ILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,908
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                                                     APPLICATION NUMBER: 60/056,845
                                                                                                                                APPLICATION NUMBER: 60/057,761
                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/047,588
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LICATION NUMBER: 60/056,664
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FILING DATE: 1997-08-22
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FILING DATE: 1997-06-06
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                                                                                          LICATION NUMBER: 60/056,892
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2.0%; Score 12; DB 4; Length 27; 100.0%; Pred. No. 0.00015;

Query Match Best Local Similarity

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Search completed: May 30, 2003, 12:33:43 Job time: 28 secs
76 LDGDNVRHGLN 86
                         LDGDNVRHGLN 76
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Gaps

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Length 204;

Score 11; DB 4; Length 2v-, Pred. No. 0.0083;

Query Match Best Local Similarity 100.

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Gencore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 12:32:25; Search time 49 Seconds

(without alignments)
1270.461 Million cell updates/sec

Perfect score: 615
Sequence: 1 MSGIKKQKTENQQKSTNVVY......MAPKAWKVLTDYYRSEMDKN 615

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
Searched: 383519 seqs, 101223694 residues

Word size: 10
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31

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 1000 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Published\_Applications\_AA:\*

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14: /cgn2\_6/ptodata/1/pubpaa/USOE\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		% Query			SUMMARIES	
No.	Score	Match	Match Length DB	BB	QI	Description
Н	221	35.9	619	6	US-09-974-298-184	Sequence 184, App
2	65	10.6	65	10	US-09-864-761-39981	Sequence 39981, A
m	55	9.9	174	6	US-09-809-391-635	Sequence 635, App
4	38	6.2	624	6	US-09-984-245-196	
5	38	6.2	624	9	US-09-966-262-196	Sequence 196, App
9	38	6.2	624	6	US-09-983-966-196	196,
7	38	6.2	624	6	US-10-143-090-196	196,
80	38	6.2	624	10	US-09-771-161A-244	Sequence 244, App
6	36	5.9	36	6	US-09-809-391-634	Sequence 634, App
10	28	4.6	45	6	US-09-984-245-332	332,
11	28	4.6	45	6	US-09-966-262-332	332,
12	28	4.6	45	σ	US-09-983-966-332	Sequence 332, App
13	28	4.6	45	σ	US-10-143-090-332	Sequence 332, App
14	20	ж. Э.	41	6	US-09-984-245-340	340,
15	20	3.3	41	6	US-09-966-262-340	Sequence 340, App
16	20	3.3	41	6	US-09-983-966-340	340,
17	20	3.3	41	σ	US-10-143-090-340	Sequence 340, App
18	17	2.8	37	6	US-09-984-245-339	
19	17	2.8	37	6	US-09-966-262-339	339,

RESULT 2 US-09-864-761-33981 Sequence 39981, Application US/09864761 Patent No. US20020048763A1

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Sequence 339, App Sequence 153, App Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 637, Appl Sequence 338, App Sequence 338, App Sequence 338, App Sequence 338, App Sequence 338, App Sequence 338, App								1420940CD1	Length 619; Indels 0; Gaps 0;	DAEFYEHRKEERCSRVWGT 348 THITITITITITITITITITITITITITITITITITITI	PLELKOKCKEMNADAVFAF 408	LELKOKCKEMNADAVFAF 413	E .46	7) 4.	E 52	/GRDPAGMPHPETKKDLYE 533	INEFDFISGTRMRKLAREG 588	INEFDFISGTRMRKLAREG 593
US-09-983-966-339 US-10-14-090-339 US-10-156-239-40 US-10-19-485-40 US-09-715-6233-40 US-09-981-391-637 US-09-981-245-338 US-09-983-966-26-338 US-10-14-090-338	ALIGNMENTS	9974298	EXPRESSED IN BREAST CANCER	6/60	238,331			No. US20020156263A1	Score 221; DB 9; Len Pred. No. 1.6e-206; 0; Mismatches 1; I	DGVINMSIPIVLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGT 	TCTKHPHIKMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAF	TCTKHPHIKMYMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAF	OLRNPVHNGHALLMODTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEE	KKLLEKGI KHPV LLLHPLGGWTKL	GVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLY!	YAGPTEVQWHCRSRMIAGANFYIV	PTHCGKVLSMAPGLISVEIIPFRVAAVNKAKKAMDFYDPARHNEFDFISGTRMRKLAREG	PTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREG
88 37 9 33 162 9 33 162 9 33 162 9 33 162 9 00 39 9 00 39 9 00 39 9		ication US/0997 156263A1	ei-Mei GENES		NUMBER: 60/238, : 2000-05-10 NOS: 194	ogram	sapiens	feature . ON: Incyte ID	35.9%; larity 99.7%; Conservative	SIPIVLPVSAED 	HIKMVMESGDWL	HIKMVMESGDWL	HNGHALLMQDTC	ниснасьмортк	STIVALEPSPMLY	STIVALEPSPML	VLSMAPGLTSVE	VLSMAPGLTSVE
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		SULT 1 -09-974-298-184 Sequence 184, Application Patent No. US20020156263A1	Chen, Chen, NVENTIC	T FILING DA	APPLICATION NUMBER: FILING DATE: 2000-0 ? OF SEQ ID NOS: 194		RT M: Homo	KEY: misc_ INFORMATI -298-184	imi ;	289 DGVINE        294 DGVINE	349 ТСТКНЕ	354 TCTKHE	60		469 GVLDPK	474 GVLDPK	529 PTHGGK	534 PTHGGK
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55 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGK 109
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                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.9%; Score 55; DB 9; Length 174; Best Local Similarity 100.0%; Pred. No. 2e-45; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: Z001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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APPLICATION NUMBER: PCT/US98/05311
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PPLICATION NUMBER: US 60/041,277
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/042,344
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FILING DATE: 1997-03-21
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APPLICATION NUMBER: US 60/048,188
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,094
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FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
                                                                                                                                              Sequence 635, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
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Patent No. US20020165374A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/154,707
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-809-391-635
  SPFAK 127
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SPFAK 65
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LENGTH: 174
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                                                                            APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 EEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFI 122
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BE292722.1, EVALUE 4.00e-32
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BONE MARROW, SIGNAL = 1.
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SEQ ID NO 39981
LENGTH: 65
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                                                                                                                                            FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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LING DATE: 2001-01-30
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                                                                                                                                                                                                                                FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2000-08-03
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APPLICATION NUMBER: US 60/234,687
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FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                     PLICATION NUMBER: GB 24263.6
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                                                               Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER:
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NUMBER OF
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FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/048,186

FILING DATE: 1997-05-30

PRIOR

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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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CURRENT APPLICATION NUMBER: US/09/983,966
CURRENT APPLICATION NUMBER: US/09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,261
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR PRILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR PILING DATE: 1997-05-30
PRIOR PAPLICATION NUMBER: US 60/048,160
PRIOR PILING DATE: 1997-05-30
PRIOR PAPLICATION NUMBER: US 60/048,160
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-06-30
PRIOR PILING DATE: 1997-08-05
PRIOR PILING DATE: 1997-08-05
PRIOR PILING DATE: 1997-08-05
PRIOR PILING DATE: 1997-08-19
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SEQ ID NO 196
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US-09-966-262-196
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Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 38; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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PRIOR FILING DATE: 1997-08-05
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
                                                                                                                                                                                            APPLICATION NUMBER: US 60/048,096
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,355
FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,154
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/054,804
FILING DATE: 1997-08-05
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APPLICATION NUMBER: US 60/041,276
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,281
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,187
FILING DATE: 1997-05-30
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FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/042,344
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APPLICATION NUMBER: US 60/048,350
          APPLICATION NUMBER: US 60/048,069
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APPLICATION NUMBER: US 60/048,094
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                                                                                                    LING DATE: 1997-05-30
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; ORGANISM: Homo sapiens
US-09-984-245-196
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    0; Indels
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                                              20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                     30 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 67
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                                                                                                                                                                                                                                                             APPLICANT: LEVINE, et al.
TILLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILLE REPERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILLING DATE: 2001-01-26
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION UNMER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
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100.0%; Pred. No. 1...
1... 0; Mismatches
  0; Mismatches
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; Publication No. US20030049618A1
; GENERAL INFORMATION:
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  38; Conservative
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Matches 38; Conservative
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Matches 36; Conservative
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ORGANISM: Homo sapiens
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US-09-984-245-332
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Best Local Similarity 100.0%; Pred. No. 2.16-28;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REPERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
                                                       PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR PELLING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE: 1997-05-30 PLICATION NUMBER: US 60/048,160
APPLICATION NUMBER: US 60/048,135
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,355
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LICATION NUMBER: US 60/048,351
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                                       us 60/050,937
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Publication No. US20030069406A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PATENTIN VOR. 2.0
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NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 624
EBROTH: 624
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US-10-143-090-196
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APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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                                                          Sequence 332, Application US/09966262 Publication No. US20030050461A1
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SOFTWARE: PatentIn Ver.
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CORGANISM: Homo sapiens
US-09-966-262-332
                                                                                      GENERAL INFORMATION:
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100.0%; Pred. No. 1.2e-1
APPLICANT: Young et al.
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                                                        CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US98/05311
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IOR APPLICATION NUMBER: US 60/042,344
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APPLICATION NUMBER: US 60/048,094
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APPLICATION NUMBER: US 60/048,350
FILING DATE: 1997-05-30
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LICATION NUMBER: US 60/048,188
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APPLICATION NUMBER: US 60/050,937
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APPLICATION NUMBER: US 60/048,187
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APPLICATION NUMBER: US 60/048,099
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PRIOR APPLICATION NUMBER: US 60/048,352
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APPLICATION NUMBER: US 60/048,186
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,131
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APPLICATION NUMBER: US 60/048,096
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PRIOR APPLICATION NUMBER: US 60/048,355
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PRIOR FILING DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
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LICATION NUMBER: US 60/041,281
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PRIOR APPLICATION NUMBER: US 60/048,154
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PRIOR FILING DATE: 1997-10-02
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PRIOR FILING DATE: 1998-09-17
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Best Local Similarity 100.0
Matches 28; Conservative
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; ORGANISM: Homo sapiens
US-09-984-245-332
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Score 28; DB 9; Length 45; Pred. No. 1.2e-19;

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Publication No. US20030069406A1
GENERAL INFORMATION:
STILLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PS2004P1
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PACENTIN VET. 2.0
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Pred. No. 1.2e-19;
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100.0%; Pred. No. 1.2e-19
tive 0; Mismatches (
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
                                                                           Query Match 4.6%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 28; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-10-29
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
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PILING DATE: 1997-03-21
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APPLICATION NUMBER: US 60/041,276
APPLICATION NUMBER: US 60/041,281
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APPLICATION NUMBER: US 60/048,094
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Patent No. US20020165374A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 28; Conservative
                       ORGANISM: Homo sapiens
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US-09-984-245-340
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US-10-143-090-332
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IITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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                                    20 YQAHHVSRNKRGQVVGTRGGFRGCTVWL 47
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PRIOR APPLICATION NUMBER: PCT/US98/05311
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APPLICATION NUMBER: US 60/041,277
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LICATION NUMBER: US 60/041,276
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LICATION NUMBER: US 60/048,350
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LICATION NUMBER: US 60/048,095
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PAPLICATION NUMBER: US 60/048,131
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,096
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FILING DATE: 1997-05-30
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LICATION NUMBER: US 60/041,281
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LICATION NUMBER: US 60/048,094
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LICATION NUMBER: US 60/050,937
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LICATION NUMBER: US 60/048,187
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PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
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APPLICATION NUMBER: US 60/048,351
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APPLICATION NUMBER: US 60/048,154
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PRIOR APPLICATION NUMBER: US 60/048,188 PRIOR FILING DATE: 1997-05-30 PRIOR FILING DATE: 1997-05-30 PRIOR PLING DATE: 1997-05-30 PRIOR PELING DATE: 1997-05-30 PRIOR PELING DATE: 1997-05-30 PRIOR PELING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,099 PRIOR PELING DATE: 1997-05-30 PRIOR PELING DATE
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 20; Conservative
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LENGTH: 41
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GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRENT APPLICATION NUMBER: US/09/966,262
RRENT FILING DATE: 2001-10-01
                                                                                                                     APPLICATION DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,186
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IOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/048,095
FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/048,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/048,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,160
FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/048,096
FILING DATE: 1997-05-30
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IOR APPLICATION NUMBER: US 60/041,276
IOR FILING DATE: 1997-03-21
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                                             LICATION NUMBER: US 60/048,099
                                                                        FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,352
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/048,069
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FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/048;154
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PRIOR APPLICATION NUMBER: US 60/054,804
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PRIOR APPLICATION NUMBER: US 60/056,370
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PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
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Publication No. US20030050461A1
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                                                                                                                                                                                                                                                                              FILING DATE: 1997-05-30
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Best Local Similarity 100.09
Matches 20; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-984-245-340
                                                                                                                                                                                                                                                                                                                                                                                                              DATE:
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Length 41; Indels

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OM protein - protein search, using sw model

May 30, 2003, 12:28:05; Search time 43 Seconds (without alignments) 1374.946 Million cell updates/sec Run on:

US-09-898-165B-7 615 1 MSGIKKQKTENQQKSTNVYY......MAPKAWKVLTDYYRSEMDKN 615 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283224 seqs, 96134422 residues Searched:

10 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	adenylyl-sulfate k	sulfâte adenylyltr		sulfate adenylyltr	$\overline{}$	probable sulfate a	sulfate adenylyltr			sulfate adenylyltr	3'-phosphoadenosin	(1)	adenylylsulfate ki			probable adenylyl-	adenylyl-sulfate k	adenylyl-sulfate k	ATP sulfurylase, l	hypothetical prote	adenosine 5'-phosp	adenylyl-sulfate k	adenylyl-sulfate k	hypothetical prote	adenyly1-sulfate k	~	. adenylyl-sulfate k		adenosine 5'-phosp
SUMMAKIES	ŢĮ	JW0087	S44079	S44267	T01204	JC4383	T08594	E71409	T52659	S44943	T14475	T24918	S74917	T50101	S47640	T06100	H95932	ZZZRNQ	E95320	G82672	C55228	H83472	S18729	T08076	A87433	AD3471	691	B65056	D91079	E85924
	DB	-	~	7	Н	Н	~	~	7	7	7	٦	7	7	Н	7	7	-	?	7	~	7	Н	~	2	7	7	Н	7	7
	Length	624	424	463	489	610	459	465	469	476	483	652	177	202	276	293	633	641	641	099	110	196	214	312	635	644	200	201	201	201
æ	Query Match				3.6	•	3.4	3.4	3.4	3.4		2.9	•	•	•			2.0	•	2.0	•	1.8	1.8	1.8	1.8	1.8	1.6	1.6	1.6	1.6
	Score	38	22	22	22	22	21	21	21	21	21	18	13	13	12	12	12	12	12	12	11	11	11	11	11	11	10	10	10	10
	Result No.	1	7	e	4	2	9	7 .	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

δž Dp

adenosine 5-phosph adenylyl-sulfate k adenylylsulfate ki	ALIGNMENTS	2.7.1.25) - human 5.7.1.25) - human 5.5'-phosphosulfate kinase; PAPS kinase (EC 2.7.1.25); sulfate adenylyltransferase (EC 1) 6revision 23-Apr-1999 #text_change 03-Jun-2002 7.7.; Sulko, M.; Takami, Y.; Nakayama, T.; Nakajima, J.	1998 cterization of the human bi MID:9648242	378100; PIDN:AAC28429.1; PID:93378101 e catalyzes the phosphorylation of adenylyl	lyzes nosul fing; ASK> (ogy	re 38; DB 1; Length 624; ed. No. 2e-30; Mismatches 0; Indels 0; Gaps 0;	YQAHHVSRNKRGOVVGTRGGFRGCTVWLTGLSGAGKTT 57 	) met3-1 - potato 10-Nov-1995 #text_change 16-Jul-1999 1. Riesmeier, I.W.	C C C C C C C C C C C C C C C C C C C	1342; PIDN:CAA52953.1; PID:9531495 se met3-1; sulfate adenylyltransferase homo rase homology <sat></sat>	re 22; DB 2; Length 424; ed. No. 4.6e-14; Mismatches 0; Indels 0; Gaps 0;
AH0856 AF0408 F82062	ALIG	25) - osphos (EC 2 sion 2	62, 1037-1040, sion, and chara UID:98312048; E	NID:93	yltransfe adenosine me; nucle kinase l ng motif yltransfeer) (cove	Scc Pr 0;	GGFRGCTVI                GFRGCTVI	2.7.7.4) met3-1 tato) vision 10-Nov-1	ization	X75041; NID:g471342; enylyltransferase me ansferase adenylyltransferase	Sco Pr 0;
0,00		.7.1. 5'-ph inase _revi	62, sion UID	26; fate	nyl pho nzyl ate ndi nyl	6.2%; 100.0%; ive	GTR GTR GTR	(EC (Po	ter	41; ylt era yly	68; 08
201 213 215		(EC sine ate (man uenc	Biochem.  G, expres  JW0087; M	GB:AF033026; e: Brain enylylsulfate	ate ade 3'-phos ional e lylsulf tide-bi ate ade	vat	NKRGOVV         NKRGOVV	erase ( erosum equence 44079	994 charac 7497; M	> BL:X750 adenyl ltransf te aden	3.6%; larity 100.0%; Conservative
1.6 1.6		□ 10 H 0	nol. Bio loning, ber: JW0 3087 : mRNA	ces: GB:AF033 source: Brain KKF> as adenylylsu	as sulfi animal tifunct: adeny nucleo n: sulfi	넡	QAHHVSR            QAHHVSR	ltransfenum tub 1994 #sc 7497; Schen	112, 1 lon and ber: S6 7497 minary	24 <klo ces: EM sulfate leotidy : sulfa</klo 	h Similarity 22; Conser
, 10 10 10		SULT 1 0087 enylyl-sulfate kinase Alternate names: adeno Contains: adenylylsulf Species: Homo sapiens Date: 23-Apr-1999 #seq Accession: JW0087 Accession: JW0087	osci. Biotechnol. Title: CDNA clonir Reference number: Accession: JW0087 Molecule type: mR	ren al <as< td=""><td>CSZ</td><td>Match ocal Sir s 38;</td><td>20 YÇ  </td><td>adenylyltransferase ss: Solanum tuberosum 07.5ep-1994 #sequenc in: S67497; 844079</td><td>6, 105 Isolationse numlion: S6': prelint</td><td>es: 1-4 referencs: cs: met3-1 amily: ds: nuc.</td><td>atc</td></as<>	CSZ	Match ocal Sir s 38;	20 YÇ 	adenylyltransferase ss: Solanum tuberosum 07.5ep-1994 #sequenc in: S67497; 844079	6, 105 Isolationse numlion: S6': prelint	es: 1-4 referencs: cs: met3-1 amily: ds: nuc.	atc
30 31 32		RESULT 1 JW0087 adenyly1-sulfe N,Alternate ne N,Alternate ne C,Species: Hon C,Date: 23-Apr C,Accession: C	Biosci. 1 A;Title: A;Refere: A;Access: A;Molecul A;Residue	A; Cross-referer A; Experimental C; Function: <as A; Description:</as 	C; Function: A; Description C; Superfamil. C; Keywords: F; 52-215/Domm F; 59-66/Regis F; 226-620/Dom F; 133/Bindin	Query Match Best Local 8 Matches 38	Qy	RESULT 2 S44079 sulfate a C;Species C;Date: (C;Access	A) Reference A) Reference A) Access A) Status A) Molecus	A; Residues: 1-424 <klo> A; Cross-references: EMBL:X75041; NID:g471342; C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: sulfate adenylyltransferase mec; Keywords: nucleotidyltransferase F;11-409/Domain: sulfate adenylyltransferase</klo>	Query M Best Lo Matches

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Ajdene: papss
Cjruction: ASKF>
Cjruction: ASKF>
Cjruction: as adenylylsulfate kinase catalyzes the phosphorylation of adenylylsul
Cjruction: ASATF>
AjDescription: as adenylyltransferase catalyzes the reaction of sulfate and A
AjDescription: as sulfate adenylyltransferase catalyzes the reaction of sulfate and A
AjDescription: as sulfate adenylyltransferase catalyzes the reaction of sulfate and A
Cjruction: as sulfate adenylyltransferase homology ASK>
Fig. 37-200/Domain: adenylylsulfate kinase homology ASK>
Fig. 37-200/Domain: adenylylsulfate kinase homology ASK>
Fig. 111/Domain: 3'-phosphoadenosine-5'-phosphosulfate binding #status predicted APA
Fig. 111/Domain: sulfate adenylyltransferase homology ASAT>
Fig. 118/Binding site: phosphate (Ser) (covalent) #status predicted
A;Title: A multifunctional Urechis caupo protein, PAPS synthetase, has both AIP sulfu A;Reference number: JC4383; MUID:96096529; PMID:8522184 A;Accession: JC4383
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T.M.; Terryn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U68218; NID:91527218; PIDN:AAB53100.1; PID:91527219
A;Experimental source: cv. Falcon; senescing leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS3) - Arabidopsi Nylternate names: ATP sulfurylase C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Spatiety: columbia
C; Date: 03-Aug.1998 #sequence_revision 03-Aug.1998 #text_change 20-Jun-2000 C; Accession: E71409; 568201
C; Bargka P; Wedler, H; Wedler, E; Wambutt, R; Weitzenegger, T; Pohl, T.M.; Terr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable sulfate adenylyltransferase (EC 2.7.7.4) - rape
C;Species: Basasica napus (rape)
C;Date: 11-Jun.1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08594
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                                                                         A;Molecule type: mRNA
A;Residues: 1-610 <ROS>
A;Cross-references: GB:L39001; NID:g705384; PIDN:AAB00139.1; PID:g705385
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Buchanan-Wollaston, V.; Ainsworth, C.
Plant Mol. Biol. 33, 821-834, 1997
A;Title: Leaf senescence in Brassica napus: cloning of s
A;Reference number: 216446; MUID:97260386; PMID:9106506
A;Accession: T08594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pre-
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Matches 22;
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                                                                                                          C.Species: Soldnum. C.Species: Soldnum. C.Species: Soldnum. C.Species: 08-Sep-1994 #sequence_revision. C749498, 44267
C.Accession: S67498, 4A267
C.Accession: S67497, Willmitzer, L.; Riesmeier, J.W.
Plant J. 6, 105-112, 1994
A.Title: Isolation and characterization of two cDNA clones encoding ATP-sulfurylases from A.Reference number: S67497; MUID:95004649; PMID:7920699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: met3-2
C;Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology
C;Keywords: chloroplast; nucleotidyltransferase
F;50-448/Domain: sulfate adenylyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Description: catalyzes activation of sulfate to adenylyIsulfate C; Superfamily: sulfate adenylyItransferase met3-1; sulfate adenylyItransferase homology C; Keywords: nucleotidyItransferase F;70-473/Domain: sulfate adenylyItransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenylyl-sulfate kinase (EC 2.7.1.25) - spoonworm (Urechis caupo)
N;Alternate names: adenosine 5'-phosphosulfate kinase; PAPS
N;Contains: adenylylsulfate kinase (EC 2.7.1.25); sulfate adenylyltransferase (EC 2.7.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribolchi, A.; Petrucco, S.; Foroni, C.; Tenca, G.L.; Ottonello, S. submitted to the EMBL Data Library, July 1997
A:Description: Sulfate permease and ATP sulfurylase mRNA are coordinately modulated in A;Reference number: Z14260
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-489
A; Cross-references: EMBL: AF016305; NID: 92738749; PIDN: AAB94542.1; PID: 92738750
A; Experimental source: cultivar Paulo; root
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: T01204
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C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 03-Jun-2002
C;Accession: JG4383
R;Rosenthal, E.; Leustek, T.
                                                                                                                                                                                                                                                                                                                             A.Status: preliminary
A.Molecule type: mRNA
A.Rosidues: 1-463 < KLO>
A.Stross-references: EMBL:X79053; NID:g479089; PIDN:CAA55655.1; PID:g479090
C.Genetlcs:
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Pred. No. 5e-14;
                                                                                           sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato
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100.0%; Pre
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:ive 0;
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Best Local Similarity 100.9
Matches 22; Conservative
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Best Local Simi
Matches 22;
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R;Murillo, M.; Leustek, T. Arch. Blochem. Blophys. 323, 195-204, 1995
Arch. Blochem. Blophys. 323, 195-204, 1995
A;Title: Adenosine-5'-triphosphate-sulfurylase from Arabidopsis thaliana and Escherizine-5'-triphosphate-sulfurylase cDNAs from Arabidopsis thaliana and analysis of a recal, Reference number: S68024; MUID:96019964; PMID:7487067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homolocikeywords: chloroplast; nucleotidyltransferase
E;1-62,Domain: transit peptide (chloroplast) **tatus predicted <TNP>
F;63-476/Product: sulfate adenylyltransferase met3-1 **status predicted <MAT>
F;64-462/Domain: sulfate adenylyltransferase homology <SAT>
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                                                                                                                met3-1 precursor - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06276; NID:g1228103; PIDN:AAA92351.1; PID:g1228104 A;Experimental source: clone APS2 C;Genetics:
                                                                                                                                        NyAlternate names: ATP sulfurylase; sulfate adenylyltransferase APS2 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 06-0ct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999 C; Accession: S4943; S68024; S68202 R; Klonus, D. Submitted to the EMBL Data Library, May 1994 A; Description: ATP-sulfurylase CDNA clone from A.thaliana. A; Reference number: S44943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sulfate adenylyltransferase (EC 2.7.7.4) ASBo precursor - wild cabbage N.Alternate names: ATP sulfurylase C;Species: Brassica oleracea (wild cabbage) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000 C;Accession: T14475 R;Hatzfeld, Y.; Logan, H.M.; Cathala, N.; Davidian, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA55799.1; PID:9487404
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A;Molecule type: DNA
A;Residues: 1-483 < LHAT>
A;Cross-references: EMBL:U69694; NID:g1589912; PID:g1589913
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Pred. No. 5.6e-13;
); Mismatches 0;
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Pred. No. 5.6e-13;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-476 <KLO>
A;Cross_references: EMBL:X79210; NID:g487403;
                                                                                                                sulfate adenylyltransferase (EC 2.7.7.4)
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100.08; Pr.
0;
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Conservative 0;
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nes 21; Conserv
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Best Local Similarity
Matches 21; Conserv
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A; Residues: 1-476 <MUW>
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C;Species: A.Cocssion: T52659
R;Hatzfeld, Y: Lee, S:: Lee, M.; Leustek, T.; Saito, K.
Gene 248, 51-58, 2000
A;Title: Functional characterization of a gene encoding a fourth ATP sulfurylase isoform
A;Reference number: 226165
A;Title: Functional characterization of a gene encoding a fourth ATP sulfurylase isoform
A;Reference number: 226165
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-469 <AMT>
A;Residues: 1-469 <AMT>
A;Residues: 1-469 <AMT>
A;Residues: 1-469 <AMT>
A;Gene: aps4
                                                    Acute 2), 403-405, 429.

Acute 2), 403-405, 420.

Acute 2), 403-405, 420.

Enhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anserbic 2, Chalwatzis, N.

A; Title: Analysis O.

A; Reference number: A71400; MUID:98121113; PMID:9461215

A; Reference number: A71400; MUID:98121113; PMID:9461215

A; Reference number: A71400

A; Reference number: A71400

A; Residues type: DNA

A; Residues: 1-465 - ABV)

A; Reference number: S68024; MUID:96019964; PMID:7487067
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A;Accession: S68201
A;Accession: SmB: U06275; NID: 9459143; PIDN: AAA92350.1; PID: 9459144
A;Cross-references: EMB: U06275; NID: 9459143; PIDN: AAA92350.1; PID: 9459144
C;Genetics: A;Amp position: 4COP9-4G3845
A;Genome: nuclear
C;Superfamily: sulfate ademylyltransferase met3-1; sulfate ademylyltransferase
C;Keywords: chloroplast; nucleotidyltransferase met3-1; sulfate ademylyltransferase
E;1-50/Domain: transit peptide (chloroplast) #status predicted <TNP>
E;1-60/Domain: sulfate ademylyltransferase homology <SAT>
F;52-450/Domain: sulfate ademylyltransferase homology <SAT>
Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
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5.4e-13; Indels
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Pred. No. 5.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 ADAVFAFQLRNPVHNGHALLM 264
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100.0%; Pre
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л, Т.; Hempel, S.; К
391, 485-488, 1998
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A)Cross-references: EMBL:X75782; NID:g414736; PIDN:CAA53426.1; PID:g414737
A;Note: it is uncertain whether Met-1, Met-14 or Met-26 is the initiator
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.
A;Reference number: 214680
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R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y
M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL158056; PIDN:CAB76273.1; GSPDB:GN00066; SPDB:SPAC1782.11
A;Experimental source: strain 972h(-); cosmid c1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AC004705; NID: 93252804; PIDN: AAC24182.1; PID: 93252812
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C; Accession: S47640; T02601; A84521; S38587
R; Arz, H.E.; Gisselmann, G.; Schiffmann, S.; Schwenn, J.D.
Biochim. Biophys. Acta 1218, 447-452, 1994
A; Title: A cDNA for adenylyl sulphate (APS)-kinase from Arabidopsis thaliana. A; Reference number: S47640; MUID:94325358; PMID:8049272

    fission yeast (Schizosaccharomyces pombe)

                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: T50101
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
R;Wood, V.; Rajandream, A.; Barrell, B.G.; Brown, S.; Harris, D.
A;Reference number: 225037
                                                    Gaps
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C;Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
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Pred. No. 4.5e-05;
        ed. No. 4e-05;
Mismatches 0;
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            Pred.
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A;Molecule type: DNA
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Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
    100.08;
                                                                                                                                                                                                                                                                                                                                                                                          adenylylsulfate kinase [imported]
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                                                                                                                                                                                             WLTGLSGAGKTTI 21
                                            13; Conservative
                                                                                                                    46 WLTGLSGAGKTTI
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    Best Local Similarity
Matches 13; Conserv
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A; Residues: 1-276 <ARZ>
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R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function: <SATE>

C; Function: <SATE>

C; Function: <SATE>

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C; Function: 
C; Fu
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C;Function: <SATF>
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A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .t.oss-reierences: EMBL:268880; PIDN:CAA93098.1; GSPDB:GN00022; CESP:T14G10.1
Experimental source: clone T14G10
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
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N;Alternate names: protein slr0676
C;Species: Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                         22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 19-Jan-2001
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C;Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
C;Superfamily: P-loop; phosphotransferase; purine nucleotide binding
F;S-164/Domain: adenylylsulfate kinase homology CASK>
F;12-19/Region: nucleotide-binding motif A (P-loop)
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9.3e-10;
hes 0; Indels
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A; Accession: S74917
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                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, January 1996
A;Reference number: Z19954
A;Accession: T24918
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LLLHPLGGWTKDDDVPLD 456
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C; Species: Caenorhabditis elegans
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Residues: 1-652 <WIL>
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A; Residues: 1-276 <STO>

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adenyly1-sulfate kinase (EC 2.7.1.25) [validated] - Arabidopsis thaliana (S.Speciess Arabidopsis thaliana (mouse-ear cress) (S.Speciess: Arabidopsis thaliane (mouse-ear cress) (S.Species: 14-May-1999 #text_change 03-Jun-2002 (S.Accession: T06100; T52055 (S.Spevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.Xsubmitted to the Protein Sequence Database, March 1999
A;Cross-references: GB:AE002093; NID:g3252812; PIDN:AAC24182.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:AL035708
A;Experimental Source: cultivar Columbia; BAC clone T5J17
R;Arz, H.E.; Gisselmann, G; Schlffmann, S.; Schwenn, J.D.
Biochim. Biophys. Acta 1218, 447-452, 1994
A;TitLe: A cDNA for adenylyl sulphate (APS)-kinase from Arabidopsis thaliana.
A;Reference number: S47640; MUID:94325358; PMID:8049272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  A.Genome: nuclear
A.Genome: nuclear
A.Introns: 66/1; 113/1; 163/1; 202/3; 231/1; 246/3
C.Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
C.Keywords: ATP; P-loop; phosphotransferase; purine nucleotide binding
F.1-37/Domain: transit peptide (chloroplast) #status predicted <INP>
F.38-276/Product: adenylylsulfate kinase #status predicted <MAT>
F.101-262/Domain: adenylylsulfate kinase homology <ASK>
F.108-115/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: EC 2.7.1.25 [validated, MUID:94325358]
C; Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
C; Keywords: ATP; P-loop; phosphotransferase; purine nucleotide binding
F;115-279/Domain: adenylylsulfate kinase homology <ASK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 276; 0.00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 293; 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-293 <ARZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF043351; PIDN:AAC39520.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 12; DB 100.0%; Pred. No. 0.00 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 12; DB 100.0%; Pred. No. 0.C ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
A; introns: 78/1; 177/1; 216/3; 245/1; 260/3
A; Note: TSJ17.110
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; Property 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 LDGDNVRHGLNR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 LDGDNVRHGLNR 87
                                                               ;Gene: At2g14750; F26C24.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T06100
A; Molecule type: DNA
A; Residues: 1-293 <BEV>
                                                                                                  A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: akn2
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Gaps

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0; Indels

Search completed: May 30, 2003, 12:33:08 Job time : 44 secs

76 LDGDNVRHGLNR 87

ò q



# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 30, 2003, 12:21:10 ; Search time 24 Seconds (without alignments) 1062.831 Million cell updates/sec Run on:

US-09-898-165B-7 615 1 MSGIKKOKTENQOKSTNVVY.....MAPKAWKVLTDYYRSEMDKN 615 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

112892 seqs, 41476328 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

21

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	% Query Match Length DB	DB	ID	Description
	509	82.8	614	<u> </u>	PPS2_HUMAN	095340 h bifunctio
7	81	13.2	621	H	PPS2_MOUSE	088428 m bifunctio
m	38	6.2	624	Н	PPS1_CAVPO	054820 c bifunctio
4	38	6.2	624	1	PPS1_HUMAN	043252 h bifunctio
5	38	6.2	624	Н	PPS1_MOUSE	Q60967 m bifunctio
9	15	2.4	206	,–ι	KAPS_EMENI	Q92203 emericella
7	15	2.4	211	٦	KAPS_PENCH	Q12657 penicillium
<b>œ</b>	13	2.1	177	П	CYSC_SYNY3	P72940 synechocyst
6	12	2.0	276	-	KAP1_ARATH	Q43295 arabidopsis
10	12	2.0	293	Н	KAP2_ARATH	049196 arabidopsis
. 11	. 12	2.0	623	Т	CYSN_XYLFA	09pd78 x cysn/cysc
. 12	12	2.0	632	П	NODQ_RHITR	ч
, 13	12	2.0	633	Н	NODQ_RHISB	007309 r nodg bifu
. 14	12	2.0	641	Н	NODQ_RHIME	P13442 r nodg bifu
15	12	2.0	646	Н	NODO_RHIS3	P72339 r nodg bifu
16	11	1.8	110	Н	YFMT_THETH	P43520 thermus the
17	11	1.8	196		CYC1_PSEAE	P57702 pseudomonas
18	11	1.8	214	-	CYC2_PSEAE	P29811 pseudomonas
19	11	1.8	312	Н	KAPS_CATRO	049204 catharanthu
20	10	1.6	200	П	CYSC_ECOLI	P23846 escherichia
21	10	1.6	215	П	CYSC_VIBCH	. Q9kp21 vibrio chol

## ALIGNMENTS

```
RESULT 1
PPS2_HUMAN
ID PPS2_HUMAN STANDARD; PRT; 614 AA.
AC 095340: 09UR30; 09BZL2; 09P0G6; 09UHM1; 09UKD3; DT 30-MAY-2000 (Rel. 39, Created) , DT 15-JUN-2002 (Rel. 41, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update)
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610
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 121
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                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                   produced by alternative splicing.
--- TISSUE SPECIFICITY: EXPRESSED IN CARTILAGE.
--- DISEASE: DEFECTS IN PAPSS2 ARE THE CAUSE OF SPONDYLOEPIMETAPHYSEAL DYSPLASIA, PAKISTANI TYPE (SEMD), AN AUTOSOWAL RECESSIVE DISEASE.
THIS FORM OF SEMD IS CHARACTERIZED BY A DYSPLASIA THAT IS PRIMARILY EPIPHYSEAL WITH ONLY MILD METAPHYSEAL ABNORMALITIES.
--- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
          PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS.

ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSGIKKOKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multifunctional enzyme;
                                                                                                                                          SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D -> DGMALP (IN ISOFORM B).
R -> K (IN REF. 2).
E -> G (IN REF. 3).
R -> C (IN REF. 1).
F -> L (IN REF. 2).
F 52F4B6D972DDA91E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULFATE ADENYLYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
PP-MOTIF (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family; Alternative splicing.
ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0455; apsK; 1.
Transferase; Nucleotidyltransferase; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 509;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                         JOINED.
JOINED.
JOINED.
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                                                                                                                                                     ADENYLYLTRANSFERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69500 MW;
                                                                                                                                                                                                                                                                                                                                                                  AAF12761.1;
AAF20366.2;
AAH09894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.8%;
Llarity 99.8%;
Conservative
                                                                                                                                                                                                                                                            EMBL; AF091242; AAC64583.1;
                                                                                                                                                                                                                                                                                                                                     AAF40307.2;
AAF40307.2;
 phosphoadenylylsulfate.
                                                                                                                                                                                                                                                                                                               AAF40307.
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166
361
426
567
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567
614 AA;
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609; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:8604;
                                                                                                                                                                                                                                                                                            AF160509;
                                                                                                                                                                                                                                                                                 AF313907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
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EMBL;
EMBL;
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241 AETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPIVL 300
                                                                                                                                                                                                                                                                              360
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FISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDGGVINMSIPIVL
                                                                                                                                                                                                                                                                                                      DYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAE
                                                                                                                                                                                                                                                                              PVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVM
                                                                                                                                                                                                                                                                                                                                                                        ESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPSPMLYAGPTEVOWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMODICRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKOHAAVLEEGVLDPKSTIVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activating enzymes causes murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ul Haque M.F., King L.M., Cantor R.M., Rusiniak M.E., Swank R.T., Superti-Furga A., Haque S., Abbas H., Ahmad W., Ahmad M., Cohn D.H.; "Mutations in orthologous genes in human spondyloepimetaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDLINE=98337975; PubMed=9671738;
Kurima K., Warman M.L., Krishnan S., Domowicz M., Krueger R.C. Jr.,
Devrup A., Schwartz N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A., VARIANT BM ARG-79, AND VARIANT LYS-109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 95:8681-8685(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT BM ARG-79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dysplasia and the brachymorphic mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A member of a new family of sulfate brachymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PWK; TISSUE-Spleen;
MEDLINE-98442651; PubMed-9771708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoadenylyisulfate.

PHENDAL BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BILOSYWTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS.

TISSUE SPECIFICITY: EXPRESSED IN LIVER, CARTLIAGE, SKIN AND BRAIN. DISEASE: DEFECTS IN PAPSS2 ARE THE CAUGS OF BRACHYMORPHISM (BM), A AUTOSOMAL RECESSIVE DISEASE, WHICH IS CHARACTERIZED BY ABNORMAL
        KINASE ACTIVITY, WHICH MEDIAPES TWO STPES IN THE SULFURLASE AND APS AKINASE ACTIVITY, WHICH MEDIAPES TWO STPES IN THE SULFATE ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULFATE GROUP TO ATP TO YIELD ADENOSINE 5'-PHOSPHOSULFATE (APS), AND THE SECOND STPE IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APS YIELDING 3'-PHOSPHOADENTLYLSULFATE (PAPS: ACTIVATED SULFATE DONOR USED BY SULFOTRANSFERASE). IN MAMMALS, PAPS IS THE SOLE SOURCE OF SULFATE, AS APPEARS TO BE OMLY AN INTERMEDIATE IN THE SULFATE ACTIVATION PATHWAY. MAY HAVE A IMPORTANT ROLE IN SKELETOGENESIS DURING POSTNATAL GROWTH.
                                                                                                                                              CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                       HEPATIC DETOXIFICATION, BLEEDING TIMES AND POSTNATAL GROWTH, SUCH AS DOME-SHARED SYRULL, SHORT THICK TAIL, AND SHORTENED BUT NOT WIDENED LIMES. THE ANNORMAL POSTNATAL GROWTH HAS BEEN ATTRIBUTED TO UNDERSULFATION OF CARTILLAGE PROTEOGLYCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PP-MOTIF (BY SIMILARITY).
G -> R (IN BM; ACTIVITY ABOLISHED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Nucleotidy Irransferase; Kinase; Multifunctional e
ATP-binding; Multigene family; Disease mutation; Polymorphism.
DOMAIN 1 ?211 ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 81; DB 1; Length 621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S -> F (IN REF. 2).
MISSING (IN REF. 2).
DE375F06A79EFAAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1330223; Papss2.
InterPro; IPR002891; APS kinase.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01883; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
TIGRPAMs; TIGR00455; apsK; 1.
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                                                                                                                                                                                                                                                                                                                                                                          ADENYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF052453; AAC40191.1; -. EMBL; AF085144; AAC98687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70290 MW;
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109
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NP_BIND
ACT_SITE
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CONFLICT
CONFLICT
SEQUENCE
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VARIANT
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Matches
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30-MAY-2000 (Rel. 39, Created)
31 30-MAY-2000 (Rel. 39, Created)
31 30-MAY-2000 (Rel. 39, Last sequence update)
31 40-MAY-2000 (Rel. 40, Last sequence update)
32 40-MAY-2001 (Rel. 40, Last annotation update)
33 50-MAY-2001 (Rel. 40, Last annotation update)
34 50-MAY-2001 (Rel. 40, Last annotation update)
35 50-MAY-2001 (Rel. 40, Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

STRAIN-NIH 2;

NA VENTACALLAN K.V., ARITA H., STROTT C.A.;

Nontacachalam K.V., ARITA H., STROTT C.A.;

SUBMITTED (MAY-1997) TO THE EMBL/Genbank/DDBJ databases.

SUBMITTED (MAY-1997) TO THE FIRST STEP IS THE THE SULFATE

ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULFATE

GROUP TO ATP TO YIELD ADENOSINE 5-PHOSPHOSULEATE (APS), AND THE

SECOND STEP IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APS

YIELDING 3'-PHOSPHOADENTIALSULFATE (PAPS: ACTIVATED SULFATE DONOR

USED BY SULFOTRANSFERASE). IN MAMMALS, PAPS IS THE SOLE SOURCE OF

SULFATE, APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATE

C. SULFATE, APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATED

L. SELECTIN LIGANDS IN ENDOTHELIAL CELLS (BY SIMILARITY).

L. SELECTIN LIGANDS IN ENDOTHELIAL CELLS (BY SIMILARITY).

C. I. CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-

C. I. CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-

C. I. CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PD002350; APS_kinase; 1.
Probom; PD002381; ATP-sulfurylase; 1.
TIGREAMs; TIGR00455; apsK; 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
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InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
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ATP-binding; Multigene family.
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                                                                                                                STANDARD;
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                                                                                                          PPS1_CAVPO
054820;
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RESULT 3
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DB 1; Length 624;

Score 38;

6.28;

Query Match

CATALYTIC ACTIVITY: ATP + adenylylsulfate - ADP + 3'-

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                                                                                                                                                                                                                                                                                                                PPS1_BUDGAN
04325; 043841; 075332;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
19-JUN-2002 (Rel. 41, Last annotation update)
19-J
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CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
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WEDLINE-9711554; Pubmed-9915785;
Venkatachalam K.V., Fuda H., Koonin E.V., Strott C.A.;
Venkatachalam K.V., Fuda H., Koonin E.V., Strott C.A.;
Venkatachalam K.V., Fuda H., Koonin E.V., Strott C.A.;
Site-selected mutagenesis of a conserved nucleotide binding HXGH
motif located in the ATP sulfurylase domain of human bifunctional
3'-phosphoadenosine S'-phosphoaulfate synthase.";
J. Biol. Chem. 274:2601-2604(1999)
-1- FUNCTION: BIFUNCTIONAL ENZYME WITH BOTH ATP SULFURYLASE AND APS
KINASE ACTIVITY, WHICH MEDIATES TWO STERS IN THE SULFATE
ACTIVATION PATHWAY. HE FIRST STEP IS THE TRANSFER OF A SULFATE
GROUP TO ATP TO YIELD ADENOSINE S'-PHOSPHOSULFATE (APS), AND THE
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Fetal brain;
MEDLINE-98334672; PubMed-9668121;
Wenkatachalam K.V., Akita H., Strott C.A.;
"Molecular cloning, expression, and characterization of human bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Girard J.-P., Baekkevold E.S., Amalric F., "Sulfation in high endothelialvenules: cloning and expression of human PAPS synthetase.";
FASEB J. 12:603-612(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanagisawa K., Sakakibara Y., Suiko M., Takami Y., Nakayama T., Nakayama H., Takayanagi K., Natori Y., Liu M.-C.; "cDNA cloning, expression, and characterization of the human bifunctional ATP sulfurylase/adenosine S.-phosphosulfate Kinase
                               ö
                                  Indels
                                                                                        YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                                                                                                  67
                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Adenosine-5'-phosphosulfate 3'-phosphotransfera:
phosphoadenosine-5'-phosphosulfate synthetase)].
PAPSSI OR PAPSS OR ATPSKI.
                                                                                                                           Biosci. Biotechnol. Biochem. 62:1037-1040(1998).
   Pred. No. 1e-30;
                                                                                                                                                                                                                                                                                                          624 AA
                            Mismatches
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                                                                                                                                                                                                                                                                                                          PRT;
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                            ő
100.08;
                            Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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   Best Local Similarity
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                                                                                                                                                                                                                                                                                                          PPS1_HUMAN
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1_HUMAN
                               Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation u
                         phosphoadenylylsulfate.

BAZYME REGULATION: INHIBITED BY CHLORATE.

PATHARY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION
                                                                                                                                                                   OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS.
IISSUE SPECIFICITY: EXPRESSED IN TESTIS, PRANCREAS, KIDNEY, THYMUS, PROSTATE, OVARY, SMALL INTESTINE, COLON, LEUKOCYTES AND LIVER.
ALSO EXPRESSED IN HIGH ENDOTHELIAL VENULES (HEV) CELLS AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIR (FUTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD002350; APS_Kinase; 1.
Probom; PD002381; ATP-sulfurylase; 1.
TIGRPAMS; TIGR00455; apsK: 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme; ATP-binding; Multigene family
                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE ADENYLYLTRANSFERASE FAMILY.
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PP-MOTIF (BY SIMILARITY).
H->A: LOSS OF ACTIVITY.
N->K: INCREASED ACTIVITY.
G->A: 30% DECREASE IN ACTIVITY.
H->A: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADENYLYLSULFATE KINASE.
SULFATE ADENYLYLTRANSFERASE.
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6BC4F9648016CA31 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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S -> L (IN REF. 2).
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Interpro; IPR002650; APP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
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70847 MW;
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EMBL; AF033026; AAC28429.1; -.
Genew; HGNC:8603; PAPSS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y10387; CAA71413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.28;
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624 AA;
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133
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Q60967;
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NP_BIND
ACT_SITE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way. modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoadenylylsulfate.
PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION
                                                                                                                                                                                                                                                                                                                                                                                                       "THE ISOLATION and characterization of cDNA encoding the mouse bifunctional ATP sulfurylase-adenosine 5'-phosphosulfate kinase.";
J. Biol. Chem. 270:29453-29459(1995).
I. Biol. Chem. 270:29453-19459(1995).
I. FUNCTION: BIFUNCTIONAL ENZYME WITH BOTH ATP SULFURYLASE AND APS KINASE ACTIVITY, WHICH MEDIATES TWO STEPS IN THE SULFATE ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULFATE GROUP TO ATP TO YIELD ADENOSINE 5'-PHOSPHOAULFATE (APS), AND THE SECOND STEP IS THE TRANSFER OF A PHOSPHAPE GROUP FROM ATP TO APS YIELDING 3'-PHOSPHAPES OF A PHOSPHAPE GROUP FROM ATP TO APS YIELDING 3'-PHOSPHAPES OF A PHOSPHAPE GROUP FROM ATP TO APS SILFATE: APS APPEARS IN MAMMALS, PARS IS THE SOLES SOURCE OF SULFATE.

SULFATE, APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATED IN SULFATED IN SULFATED IN THE BIOSYNTHESIS OF SULFATED IN SANDYMENT AND ANALYMENT AND ANALYMENT AND ANALYMENT ANALYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGR00455; apsK; 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme;
ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                           MEDLINE=96094345; PubMed=7493984;
Li H., Deyrup A., Mensch J.R. Jr., Domowicz M., Konstantinidis A.K.,
(EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS.
TISSUE SPECIFICITY: EXPRESSED IN THE NEONATAL BRAIN AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 624;
Pred. No. 1e-30;
Mismatches 0; Indels
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ATP (POTENTIAL).
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InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
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ProDom; PD002381; ATP-sulfurylase; 1.
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Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                           PAPSS1 OR PAPSS OR ASAPK OR ATPSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADENYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; 8
100.0%;
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                                                                                                                    musculus (Mouse)
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                 Clarke D.L., Newbert R.W., Turner G.;
"Cloning and characterisation of the APS kinase gene from
"Cloning and characterisation of the APS kinase gene from
"Seperalized (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate - ADP + 3'-
phosphoadenylylsulfate - ADP + 3'-
-!- PATHWAY: SECOND STEP IN THE SULFATE ASSIMILATION PATHWAY THAT
LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5) phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase)
                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last annotation) (Adenosine-5)
51-Mosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4%; Score 15; DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6AADD483E2BCA1CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL)
                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA
                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PD002350; APS_kinase.
Probom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4.
100.08; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 AA; 23028 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 ENIRRIAEVAKLFAD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HILLIIIIIIIIIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y08866; CAA70089.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002350; APS_kinas
TIGRFAMs; TIGR00455; apsK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penicillium chrysogenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphotransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
NP_BIND 31
ACT_SITE 105
                                                                                                                                                                                                                                                    NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAPS_PENCH
Q12657;
                                 KAPS_EMENI
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                  KAPS_EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAPS_PENCH
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RESULT
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Gaps

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0; Mismatches

Best Local Similarity 100. Matches 38; Conservative

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphosulfate 3'-phosphotransferase).

AKN1 OR AT2G14750 OR F266-4.11 OR T6B13.1.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94345022; PubMed=8066145;
Jain A., Leustek T.;
"A cDNA clone for 5'-adenylylphosphosulfate kinase from Arabidopsis
thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leustek T.; "Analysis of ATP-sulfurylase and APS-kinase genomic DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2000 (Rel. 40, Last sequence update)
Adenylylsulfate kinase 1, chloroplast precursor (EC 2.7.1.25)
kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arz H.E., Gisselmann G., Schiffmann S., Schwenn J.-D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 1; Length 177;
Pred. No. 1.8e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0455, apsK, 1.
Transferase, Kinase, Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
E24D5B5452FCD7D8 CRC64;
          BIOSYNTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1218:447-452(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                Phosphorylation; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94325358; PubMed=8049272;
                                                                                                                                                                                                                                             InterPro; IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Physiol. 105:771-772(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                          177 AA; 19674 MW;
                                                                                                                                                                                                                            EMBL; D90902; BAA16957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Landsberg erecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 WLTGLSGAGKTTI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 WLTGLSGAGKTTI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CV COlumbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAP1_ARATH
043295;
                                                                                                                                                                                                                                                                                                                                                               NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoadenylylsulfate.
PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                              Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 3:109-136(1996).
-!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7DDC4BDA867FE7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-97061201; Pubmed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AA; 23770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 ENIRRIAEVAKLFAD 112
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U39393; AAA81521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0455; apsk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
wes 15; Conserv
                                                             STRAIN-ATCC 24791;
                                         SEQUENCE FROM N.A.
NCBI_TaxID=5076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSC OR SLR0676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase;
                                                                              Foster B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYSC_SYNY3
P72940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIND
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Matches
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STRAIN-cv. Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL). FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrear A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last aequence update)
Adenylylsulfate kinase 2, chloroplast precursor (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoadenylylsulfate.
PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS
REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOSENTHETIC PATHWAY.
-1 - SUBCELLULAR LOCATION: Chloroplast.
-1 - SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                       Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                     -I- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-I- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%; Score 12; DB 1; Length 276; 100.0%; Pred. No. 0.00029; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase: Kinase: Cysteine biosynthesis: ATP-binding; Phosphorylation; Transit peptide; Chloroplast.
TRANSIT 1 37 CHLOROPLAST (POTENTIAL).
CHAIN 38 276 ADENYLYLSULFATE KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB698643AA09D811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; ' 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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AKN2 OR AT4G39940 OR T5J17.110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC004705; AAC24182.1; -
InterPro; IPR002891; APS_kinase.
Jefam; PP010583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
TIGRFAMS; TIGR00455; apsK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AA; 29787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X75782; CAA53426.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U05238; AAC50035.1; -. EMBL; U59759; AAC50034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 LDGDNVRHGLNR 146
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOSYNTHETIC PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 LDGDNVRHGLNR 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                          Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAP2_ARATH
049196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                           thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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KAP2_ARATH
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SEOUENCE FROM N.A.

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READERSE FROM TA.

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RAY MEDLIFE-20083468 Pubbled-10617198;

RAYEL M. Dusetenbeft A. Stiekema W., Entian K. D., Terryn N.,

RAY Harris B., Ansorge W., Brandt P. Grivell L.A., Rieger M.,

RAYEL M. Dusethoeft A., Stiekema W., Entian K. D., Terryn N.,

RAY Harris B., Ansorge W., Brandt P. Grivell L.A., Rieger M.,

RAY HOLLSEN, WELLE D., Perez-Alonso M., Bourry M., Bancroft I.,

RAY T. HORESEL J., Zimmenmann W., Robben J.,

RAY And Get Schuener J., Grymoprez B., Chuang Y. J., Vandenbussche F.,

RAY And Get Schuener J., Grymoprez B., Chuang Y. J., Vandenbussche F.,

RAY And Get Schuener J., Grymoprez B., Chuang Y. J., Vandenbussche F.,

RAY And Get Schuener J., Grymoprez B., Chuang Y. J., Vandenbussche F.,

RAY And Get Schuener J., Grymoprez B., Vore W., Battlean I., Robben J.,

RAY And Get Schuener J., Grymoprez B., Chuang Y. J., Vanden Daele H.,

RAY And Get Schuener J., Grymoprez B., Changer J., Hibbert H., Strau M.,

RAY Bereiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

RAY Monighan P., Klein Lankhorst R., Rose M., Haul J., Kocherer P.,

RA Dose S., de Haan M., Mazise A.C., Schaefer M., Mellar S.,

RA Dose S., de Haan M., Mazise A.C., Schaefer M., Mellar A., Pere R.,

RA Bobel C., Feld Ray M., Elechary R., Caracuberta E.,

RA Gibbons T., Weber N., Pertann B., Granderath K., Dauner D., Herzl R.,

RA Gibbons T., Weber N., Vardenbold M., Benes V., Rechber S.,

RA Gibbons T., Weber N., Vardenbold M., Barques M., Terol J., Torres A.,

RA Gibbons T., Weber N., Vardenbold M., Barques M., Terol J., Torres A.,

RA Gibbons T., Weber N., Vandenbold M., Barques M., Terol J., Torres A.,

RA Zaccaria P., Berqer C., Monfort A., Gasacuberta E.,

RA Zaccaria P., Berqer C., Monfort A., Scheder S.,

RA Zaccaria P., Berder D., Cordes M., Haung E., Scheder N., Halliar L.,

RAY And D., Schwarz S., Scholler P., Hebber S., Francs P., Bernann N.,

RAY And D., Schwarz S., Scholler P., Hebber S., Francs P., Hebrer M.,

RAY AND S., Hiller R., Scher P., Cordes M., Haul M., Marray J., Scher P., Corde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
                    Schiffmann S., Schwenn J.-D.; "Isolation of cDNA clones encoding adenosine-5'-phosphosulfate-kinase (EC2.7.1.25) from Catharanthus roseus and an isoform (akn2) from Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoadenylylsulfate.
-!- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHETIC PATHWAY.
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                        (In) Plant Gene Register PGR98-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:769-777(1999)
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana.
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FUNCTION: ATP SULFURYLASE MAY BE THE GTPASE, REGULATING ATP

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
CySN/CySC bifunctional enzyme [Includes: Sulfate adenylyltransferase]
subunit 1 (RC 2.7.7.4) (Sulfate adenylate transferase) (SAT)
sulfurylase large subunit); Adenylylsulfate kinase (RC 2.7.1.25) (APS
kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase)]
                                                                                                                                                                           ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
EMBL; AF043351; AAC39520.1; -.

EMBL; AL03708; CAB3807.1; -.

EMBL; AL161596; CAB80657.1; -.

InterPro; IPR002891; APS_Kinase.

R Pfam; PF01583; APS_Kinase; 1.

R TGRPAMS; TIGR00455; apsK; 1.

M Transferase; Kinase; Cysteine biosynthesis; ATP-binding; Phosphorylation; Transit peptide; Chloroplast.

W Phosphorylation; Transit peptide; Chloroplast.

TRANIT 1 ? 293 ADENILYLSULFARITIAL).

THANIT CHAIN ? 293 ADENILYLSULFARITIAL).
                                                                                                                                                                                                                                             2.0%; Score 12; DB 1; Length 293;
100.0%; Pred. No. 0.0003;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                        71F1AD6E9B026886 CRC64;
                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                      100.08; FIL
                                                                                                                                                                                                                        293 AA; 31977 MW;
                                                                                                                                                                                                                                                                                                                              Query Match 2.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                              76 LDGDNVRHGLNR 87
                                                                                                                                                             293
149
196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                        142
196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSNC OR XF1501
                                                                                                                                                                                                                                                                                                                                                                                                                  CYSN_XYLFA
Q9PD78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=9a5c
                                                                                                                                                                           NP_BIND
ACT_SITE
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xvlella.
                                                                                                                                                                                                                                                                                                                                                                                                     CYSN_XYLFA
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                                            (BY SIMILARITY).

(BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.

CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3' -

phosphoadenylylsulfate.

PATHWAY: FIRST AND SECOND STEPS IN THE SULFATE ACTIVATION PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2001 (Rel. 40, Last annotation update)
NodQ bifunctional enzyme (Nodulation protein Q) [Includes: Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (ATP adenosine-5'-phosphosulfate 3'-
                          OF ACTIVATED SULFATE
                                                                                                                                                                                                                                 CYSN (BY SIMILARITY).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. CYSN/NODQ SUBFAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADENYLYLSULFATE KINASE.

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ATP (POTENTIAL).

FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                          THESE REACTIONS OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE BIOSYNTHETIC PATHWAY.
SUBUNIT: HETERODIMER COMPOSED OF CYSD, THE SMALLER SUBUNIT, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRPAMS; TIGR00455; apsK; 1.

PROSITE: PS00301; BFSCTOM, GTP; 1.

Cysteine biosynthesis; Transferase; Nucleotidyltransferase; GTP-binding; Kinase; ATP-binding; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12; DB 1; Length 623;
Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULFATE ADENYLYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
C20730A365B28E94 CRC64;
SULFURYLASE ACTIVITY (BY SIMILARITY).
FUNCTION: APS KINASE CATALYZES THE SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003980; AAF84310.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002891; APS_kinase.
InterPro; IPR002891; BPS_kinase.
InterPro; IPR004161; EFTU D2.
InterPro; IPR000795; EF_GTPbind.
Pfam; PF01583; APS_kinase; 1.
Pfam; PF01581; APS_kinase; 1.
PRIME; PR00315; ELONGARNECT.
Probom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68277 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 LDGDNVRHGLNR 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LDGDNVRHGLNR 87
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623
30
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P52978;
01-0CT-1996 (
01-0CT-1996 (
16.0CT-2001 (
                                                                                                                                                                                                                                                                                                                                   FAMILY.
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ACT_SITE
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NODQ_RHISB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Folch-Mallol J.L., Marroqui S., Sousa C., Manyani H., Lopez-Lara I.M., van der Driff K.M.G.M., Haverkamp J., Quinto C., Gil-Serrano A., Thomas-Oates J., Spaink H.P., Magias M., Thomas-Oates J., Spaink H.P., Magias M., Characterization of Rhizobium tropici CIRT899 nodulation factors: the role of nodH and nodPQ genes in their sulfation."; Mol. Plant Microbe Interact. 9:151-163 (1996).

-I. FUNCTION: PROPOSED TO PROVIDE ACTIVATED SULFATE FOR TRANSFER TO NOD FACTOR. ATP SULFURYLASE MAY BE THE GTPASE, REGULATING ATP SULFURYLASE ACTIVATE STATLARRITY).

-I. FUNCTION: APS KINASE CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
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-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE APS KINASE
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Inter Pro; IPR00161; EFTU_D2.

Inter Pro; IPR004161; EFTU_D2.

Inter Pro; IPR004161; EFTU_D2.

Inter Pro; IPR00195; EF GTPbind.

Inter Pro; IPR00195; EFTU_D2; I.

Inter Pro; IPR0144; GTP_EFTU_D2; I.

Inter Pro; IPR00144; GTP_EFTU_D2; I.

Inter Pro; IPR001455; APS_Kinase; I.

Inter Pro; IPR00145; APS_Kinase; APS_Kina
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                   'Isolation and characterization of Rhizobium tropici Nod factor
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SUBUNIT: SULFATE-ACTIVATING ENZYMES, NODP AND NODQ, MAY BE
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Vanderleyden J., Martinez-Romero E.;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Plant Microbe Interact. 9:492-500(1996)
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MEDLINE=96303535; PubMed=8755625;
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MEDLINE-97002746; PubMed=8850086;
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                                              Rhizobium
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DOMAIN 1 45
DOMAIN 458 63
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                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sulfation genes.
                                              Rhizobiaceae; R
NCBI_TaxID=398;
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                                  15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
NodO bifunctional enzyme (Nodulation protein Q) [Includes: Sulfate adenylytransferase subunit 1 (EC 2.7.7.4) (Sulfate adenylate transferases) (SAT) (ATP-sulfurylase large subunit); Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase)].
                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate. CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-phosphoadenylylsulfate. SUBUNIT: SULFATE-ACTIVATING ENZYMES, NODP AND NODO, MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYSICALLY ASSOCIATED (POTENTIAL).

SINLIARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. CYSN/NODO SUBFAMILY.

SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE APS KINASE
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ATP (POTENTIAL).

FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                              Laeremans T., Coolsaet N., Verreth C., Snoeck C., Hellings N., Vanderleyden J., Martinez-Romero E.; "Functional redundancy of genes for sulphate activation enzymes in
                                                                                                                                                                                          Rhizobium sp. (strain BR816).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00301; EFACTOR GTP; 1.
Nodulation; Transferase; Nucleotidyltransferase; GTP-binding;
Kinase; ATP-binding; Multifunctional enzyme.
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 633 AA.
PRT;
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InterPro; IPR002891; APS kinase.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
Pfam; PP00009; GTP_EFTU, 1.
Pfam; PP01583; APS_kinase; 1.
Pfam; PF013144; GTP_EFTU_D2; 1.
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TIGRFAMs; TIGR00231; small_GTP; 1.
TIGRFAMs; TIGR00455; apsK; 1.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98083747; Pubmed=9421916;
                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium.
NCBI_TaxID=48291;
   STANDARD;
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ACT_SITE
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Pred. No.

100.0%;

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NP_BIND
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSyma megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
-! FUNCTION: PROPOSED TO PROVIDE ACTIVATED SULFATE FOR TRANSFER TO
NOD FACTOR. ATP SULFURYLASE MAY BE THE GTPASE, REGULATING ATP
SULFURYLASE ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NodQ bifunctional enzyme (Nodulation protein Q) [Includes: Sulfate adenylltransferase subunit 1 (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The Rhizobium meliloti host range nodo gene encodes a protein which shares homology with translation elongation and initiation factors."; Mol. Microbiol. 3:745-755(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
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SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GTP-BINDING ELONGATION EACTOR FAMILY. CYSN/NODO SUBFAMILY.

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE APS KINASE SIMILARITY: IN THE C-TERMINAL SECTION.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                           Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                 ;
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MEDLINE-89313304; PubMed-2546009;
Cervantes E., Sharma S.B., Maillet F., Vasse J., Truchet G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: SULFATE-ACTIVATING ENZYMES, NODP AND NODQ, MAY
                                      Length 633;
         696BCA683D4B3111 CRC64;
                                     DB 1; Le
0.00059;
                                                                                                                                                                                                                                                                                                    phosphotransferase)].
NODQ OR RA0469 OR SMA0857.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Rhizobium meliloti, nodP and nodQ.";
Mol. Plant Microbe Interact. 2:181-194(1989).
                                                                                                                                                                                    641 AA.
                                             100.0%; Preu. ...
SIMILARITY).
                                    Score 12;
Pred. No.
                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92288403; PubMed=2520820;
                                                                                                                                                                                                             (Rel. 13, Created)
           69279 MW;
                                     2.0%;
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                                                                                                         LDGDNVRHGLNR 505
                                                               Conservative
                                                                                                                                                                                  STANDARD;
                                                                                        76 LDGDNVRHGLNR 87
                      Query Match
Best Local Similarity
Thes 12; Conserve
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           633 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=382;
                                                                                                                                                                                                           01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-1021
                                                                                                                                                                                  NODQ_RHIME
           SEQUENCE
                                                                                                                                                                     NODQ_RHIME
                                                                                                                                                        RESULT 14
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; P800301; FFACTOR_GTP; 1.
Plasmid; Nodulation: Transferase; Nucleotidyltransferase; GTP-binding; Kinase; ATP-binding; Multifunctional enzyme; Complete proteome.

1 458 SULFATE ADENYLYL TRANSFERASE.
DOMAIN 459 641 ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROPOSED TO PROVIDE ACTIVATED SULFATE FOR TRANSFER TO NOD FACTOR. ATP SULEURYLASE MAY BE THE GTPASE, REGULATING ATP SULFURYLASE ACTIVITY (BY SIMILARITY).
-!- FUNCTION: APS KINASE CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (PV SIMILARITY).

ATP (POTENTIAL).

FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NodQ bifunctional enzyme (Nodulation protein Q) [Includes: Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylylsulfate kinase (EC 2.7.1.25) (APS Kinase) (ATP adenosine-5'-phosphosulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1E1261F04ED33A93 CRC64;
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Pred. No. 0.0006;
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                                                                                                                                                                                                                                 PIR: S14899; ZZZRNO.
INTERPRO: IPRO02891; APS.Kinase.
INTERPRO: IPRO04161; EFTU_D2.
INTERPRO: IPRO0525; Small_GTP.
Pfam, PF00009; GTP_EFTU_I.
Pfam; PF01883; APS.Kinase; I.
Pfam; PF03144; GTP_EFTU_D2; I.
ProDom; PP001283; APS.Kinase; I.
PTGRFAMS; TIGR00231; Small_GTP: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14809; CAA32914.1; -.
EMBL; M68858; AAA26343.1; -.
EMBL; AE007237; AAK65127.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoadenylylsulfate.
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NCBI_TaxID=103798;
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474
524
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es 12; Conserv
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                PHYSICALLY ASSOCIATED (POTENTIAL).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. CYSN/NODO SUBRAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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                                                                                                                                                                                                                                                                              InterPro; IPR002891; APS_kinase.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
Pfam; PP01089; APS_kinase; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
ProDom; PD002350; APS_Kinase; 1.
TIGRFAM5; TGR00455; apsK; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
Nodulation; Transferase; Nucleotidyltransferase; GTP-binding; Kinase; ATP-binding; Miltifunctional enzyme.

Ninase; ATP-binding; Miltifunctional enzyme.

DOMAIN
SULFATE-ACTIVATING ENZYMES, NODP AND NODQ, MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 646;
0.0006;
hes 0; Indels
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1DBEE1DA257FE128 CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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100.0%;
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Best Local Similarity 100.
Matches 12; Conservative
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Search completed: May 30, 2003, 12:30:43 Job time: 24 secs

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04888 zea mays (m
026128 urechis cau
096349 brassica na
02520 arabidopsis
04530 arabidopsis
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025029 brassica ju
043870 arabidopsis
095748 arabidopsis
096149 drosophila
09541 aces acyp
025501 caenorhabdi
09542 arabidopsis
09574 acenorhabdi
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08502 zea mays (m
095479 sthizobium n
098479 arabidopsis
08151 enteromorph
09571 arabidopsis
08151 enteromorph
09573 arabidopsis
081351 enteromorph
09573 arabidopsis
081351 arabidopsis
08534 asalmonella
08634 saccharomyc
08634 saccharomyc
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MEDLINE=20006854; PubMed=10559207;
Murima K., Singh B., Schwartz N.B.;
Murima K., Singh B., Schwartz N.B.;
Sulfurylase/Adenosine 5'-phosphosulfate kinase isoform SK2.";
J. Biol. Chem. 274:33306-33312(1999).
EMBL; AR173364; AAR12780.1; JOINED.
EMBL; AR173361; AAR12780.1; JOINED.
EMBL, AR173363; AAR12780.1; JOINED.
EMBL, AR173363; AAR12780.1; JOINED.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01747; APP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98337975; PubMed=9671738;
Kuriana K., Warman M.L., Krishnan S., Domowicz M., Krueger R.C. Jr.,
Kuriana K., Schwartz N.B.;
"A member of a family of sulfate-activating enzymes causes murine
brachymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
ATP sulfurylase/APS kinase isoform SK2 (EC 2.7.7.4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 95:8681-8685(1998).
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                                                                        042520
096530
023324
0987D8
092NZ9
043870
                                           Q96349
Q9ZNZ8
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Q9SBL0
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092VH6
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09S0R9
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09FJX1
09A882
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Q8REL1
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Q9P7G9
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RESULT 1
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DD 09UIR2;
DT 01-MAY-
DT 01-MAY-
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DE ATP 8ul
OC BURARYO
OC MAMMAILO
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Oggys0 mus musculu
Ogguege homo sapien
Ogbrige homo sapien
Ogotf4 homo sapien
Ogotf4 homo sapien
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Ogotf4 allium cepa
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1456.540 Million cell updates/sec
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1 MSGIKKQKTENQQKSTNVVY......MAPKAWKVLTDYYRSEMDKN 615
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                                                                                                     May 30, 2003, 12:26:25 ; Search time 87 Seconds
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         parameters:
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                                                                      OM protein - protein search, using sw model
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Q9QYS0
Q9JK86
Q9UE98
Q9P1P9
Q96TF4
Q90XY2
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Gapop 60.0 , Gapext 60.0
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Q9SDP4
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Q43183
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sp_unclassified:*
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sp_human:*
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                                                                                                Gaps
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Kurima K., Singh B., Schwartz N.B.;
"Genomic organization of the mouse and human genes encoding the ATP Sulfurylase/Adenosine 5'-phosphosulfate kinase isoform SK2.";
D. Biol. Chem. 274:33306-33312(1999).
EMBL: AF172866; AAF12760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98337975; PubMed-9671738;
Kurima K., Warman M.L., Krishnan S., Domowicz M., Krueger R.C. Jr.
Deyrup A., Schwartz N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deyrup A., Schwartz N.B.;
"A member of a family of sulfate-activating enzymes causes murine brachymorphism.";
                                                                                               ö
                                                                  23.1%; Score 142; DB 4; Length 265; 100.0%; Pred. No. 1.5e-145; .ive 0; Mismatches 0; Indels
                                      265 AA; 30142 MW; D75A237,4E40C334F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinase; Nucleotidyltransferase; Transferase.
SEQUENCE 621 AA; 70408 MW; 019519DC8E239F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase/APS kinase isoform SK2 (EC 2.7.7.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 95:8681-8685(1998).
            Nucleotidyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMEL, AF172857, ART12760.1; JOINED. BMEL, AF172859; AAF12760.1; JOINED. BMEL, AF172859; AAF12760.1; JOINED. BMEL, AF172869; AAF12760.1; JOINED. BMEL, AF172861; AAF12760.1; JOINED. BMEL, AF172863; AAF12760.1; JOINED. BMEL, AF172864; AAF12760.1; JOINED. BMEL, AF172864; AAF12760.1; JOINED. BMEL, AF172865; AAF12760.1; JOINED. BMEL, AF172865; AAF12760.1; JOINED.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD002350; APS_kinase; 1.
Probom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; APP-sulfurylase.
Pfan: PF01583; APS_kinase: 1.
Pfam: PF01747. ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                190 IIPFRVAAYNKAKKAMDEYDPA 211
                                                                                                                                                                                                                                547 IIPFRVAAYNKAKKAMDFYDPA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0455; apsK; 1
                                                                               Best Local Similarity 100. Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papss2
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1330223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6;
                           NON_TER
SEQUENCE
                                                                  Query Match
              Kinase;
                                                                                                                                                                                                                                                                                                                                            090YS0;
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                                                                                                                                                                                                                                                                                                                              090YS0
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                                                                                                                                                                                                                         169
                                                                                                                                                   109 LFADAGLVCITSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRAR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500 RMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNK 557
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
Adenosine 5'-phosphosulfate kinase/ATP sulfurylase 2.
Cavia porcellus (Guinea pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia: Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fodine FROM N.A.

Fuda H., Strott C.A.;

Fuda H., Strott C.A.;

Guinea pig bifunctional adenosine 5'-phosphosulfate kinase/ATP

"Guinea pig bifunctional big bifunctional bifunctional
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Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 11; Length 62
Pred. No. 1e-53;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016496; AAD09325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 AA; 70031 MW; 50E187D16335985A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
13.2%; Score 81; DB 11; 1 100.0%; Pred. No. 9.2e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 AA
                                  100.0%; Pred. No. 9.2 ive · 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002891; APS_Kinase.
InterPro; IPR002650; APP-sulfirylase.
Pfam: PF01583; APS_Kinase; 1.
Pfam: PF01747; ATP-sulfurylase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                          170 AGEIKGFTGIDSDYEKPETPE 190
                                                                                                                                                                                                                                                                                                   169 AGEIKGFTGIDSDYEKPETPE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deyrup A.T.;
"Human ATP sulfurylase/APS kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.4%; Sco
1 Similarity 100.0%; Pr
58; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0455; apsk; 1.
                                                                             Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP sulfurylase/APS kinase.
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                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                     81;
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TISSUE=EYE;
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EMBL, AF10527; AAF40236.1; --
INTERPIC: IPR002891; APS. kinase.
InterPro: IPR002650; ATP-sulfurylase.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            Wood T.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Lens.
                                                                                                                                                                                                                                                                                                                               MEDLINE-20145452; PubMed-10679223;
Xu Z.-H., Otterness D.M., Freimuth R.R., Carlini E.J., Woo
Mitchell S., Moon E., Kim U.-J., Xu J.-P., Siciliano M.J.,
Weinshilboum R.M.;
                                                               Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom: Freeze...
TIGRFAMS; TIGRO0455; apsK; 1.
                                          70881 MW; 0008DBC57B6F35BC CRC64;
                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3'-phosphoadenosine 5'-phosphosulfate synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3'-phosphoadenosine 5'-phosphosulfate synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 67
                                                                                                      20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                                                                 10 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                                   ö
                                                              DB 4; Le
6.2e-32;
                                                             6.2%; Score 38; DB 100.0%; Pred. No. 6.2. tive 0; Mismatches
                                                                                                                                                                                 624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 38; DB 100.0%; Pred. No. 6.2 tive 0; Mismatches
ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01583; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20145452; PubMed=10679223;
                     TIGRFAMS; TIGR00455; apsK; 1.
                                                                        Local Similarity 100.
Les 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                          624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 38; Conserv
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBL_TaxID=9606;
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                                 Kinase.
SEQUENCE
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Matches
                                                                                  Matches
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Xu Z.-H., Otterness D.M., Freimuth R.R., Carlini E.J., Wood T.C., Mitchell S., Moon E., Kim U.-J., Xu J.-P., Siciliano M.J., Weinshilboum R.M., "Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPSS1) and PAPSS2: gene Cloning, characterization and chromosomal localization."; Biochem. Biophys. Res. Commun. 268:437-444(2000).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 19, Last annotation update)
3'-phosphoadenosine 5'-phosphosulfate synthase 2.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conserved synteny between the Fugu and human PTEN locus and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21455682; PubMed=11571655;
Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner S., Tan Y.H.,
Venkatesh B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Oncogene 20:5554-5561(2001).
EMBL; AF32922: AAL08416.1; -.
Interpro; IPR002891; APS_Kinase.
Interpro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_Kinase; 1.
                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD002350; APS_kināse; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
TIGREAMS; TIGRO0455; apsk; 28E50148377C4169 CRC64;.
SEQUENCE 613 AA; 68948 MW; 28E50148377C4169 CRC64;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0455; apsK; 1.
FERNIFACE 624 AA; 70833 MW; A3DC9B943E68CDD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 YOAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Le 6.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 38; DB 100.0%; Pred. No. 6.2 live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01583; APS_kinase; 1.
Pfam; PF01747; APP-Sulfurylase; 1.
ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; APP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
                                                                                                                                                                                                                                                                                                                                                              EMBL, AF097711; AAF40235.1; JOINED.
EMBL, AF097712; AAF40235.1; JOINED.
EMBL, AF097713; AAF40235.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF097714; AAF40235.1; JOINED. EMBL; AF097715; AAF40235.1; JOINED.
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EMBL; AF097718; AAF40235.1; JOINED.
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EMBL; AF097720; AAF40235.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF097716; AAF40235.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUL-2001) to the
EMBL; AF097721; AAF40235.1;
EMBL; AF097710; AAF40235.1;
                                                                                                                                                                                                         SEQUENCE OF 22-624 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC011392; AAH11392.1
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Best Local Similarity 100.4
Matches 38; Conservative
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InterPro; IPR002650; ATP-sulfurylase.
                                                                                        Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4679;
                                                                                                                                                                                                                                                               ATP-sulfurylase.
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                                                        SEQUENCE
                                                                               Query Match
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                                                                                                                                                                                                       Q8W1X3
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                                                                                                                                                                                                                                                                                                        "Characterization of Brachyury downstream notochord genes in the Ciona intestinalis embryo."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AB036852; BAB00629-1;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
Satoh N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                  Gaps
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum (Potato).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klonus D., Hoefgen R., Willmitzer L., Riesmeier J.W.; "Isolation and characterization of two cDNAclones encoding ATP-sulfurylase from Potato by complementation of a yeast mutant."; Plant J. 6:105-112(1994).
EMBL: X75041; CAA52953.1; -.
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          Length 613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                69559 MW; 75223CCB022BC297 CRC64;
                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
(EC 2.7.7.4).
                                                                   436 PVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDP 472
                                                     437 PVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDP 473
         DB 13; LA 7.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1e-19;
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       6.0%; Score 37; DB
ilarity 100.0%; Pred. No. 7.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%; Score 26; DB
llarity 100.0%; Pred. No. 7.1
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 MNADAVFAFQLRNPVHNGHALLMQDT 428
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                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
                                                                                                                                                           Created)
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                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01747; ATP-sulfurylase; 1.
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MEDLINE-95004649; PubMed-7920699;
                                                                                                                                                                                                                                                                                                                                                                                                                          IGRFAMS; TIGRO0455; apsk; 1.
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01583; APS_kinase; 1
                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel, 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfate adenylyltransferase
                                                                                                                                                                                           ATP sulfurylase/APS kinase
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
     Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                  Ciona intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               618 AA;
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=7719;
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                                                                                                                                   Q9NDP8
Q9NDP8;
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                                                                                                              RESULT 8
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Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Asparagales; Alliaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pither-Joyce M.D., McCallum J.A.;

"Isolation of an ATP-sulfurylase CDNA clone from Allium cepa.";

"Isolation of an ATP-sulfurylase CDNA clone from Allium cepa.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF401295; AAG1615.1;

InterPro; IPR002650; ATP-sulfurylase.

Pfam; PF01747; ATP-sulfurylase; 1.

ProDom; PD00281; ATP-sulfurylase; 1.

SEQUENCE .458 AA; 51360 MW; F7A43A53F3A7F04C CRC64;
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Pither-Joyce M.D., McCallum J.A.;
"Isolation of an ATP-sulfurylase CDNA clone from Allium cepa.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR212154; ARF18998 1...
InterPro; IPR002650; ATP-sulfurylase.
Pfont; PF01747; ATP-sulfurylase.
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                                                                                                                                                            Length 424;
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                                                                                                     424 AA; 47519 MW; E82A27DC11350ABC CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                         Score 22; DB 10; 1; Pred. No. 1.1e-14;
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100.0%; Pred. No.
tive 0; Mismatch
Pfam; PF01747; ATP-sulfurylase; 1. ProDom; PD00281; ATP-sulfurylase; 1. TIGRFAMS; TIGR00339; sopr; 1. Nucleotidyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                             200 NADAVFAFQLRNPVHNGHALLM 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                         3.6%; Scc...
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                Conservative
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les 22; Conservative
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9A45FAA5133A17FF CRC64;

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InterPro; IPR002650; ATP-sulfurylase.
    51372 MW;
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                                                                                      Conservative
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                                                                                                                                                                                                                                                                            PRELIMINARY;
    463 AA;
                                             Query Match
Best Local Similarity
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NCBI_TaxID=4113
                                                                                      22;
    SEQUENCE
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Q43183
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase precursor (EC 2.7.7.4).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine.
NCBI_TAXID=3847;
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                                                                                                                             Gaps
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TRANSIT 1 48
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                                                                                  Length 461;
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EMBL, AF452454; AAL74418.1; -
SEQUENCE 461 AA; 51700 MW; 3504272C93923100 CRC64;
                                         04083BE879CBDE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                DB 10; Le
1.2e-14;
thes 0;
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Pred. No. 1.2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.6%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                   461 AA.
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                                                                                3.6%; Score 22; DB 100.0%; Pred. No. 1.2 itive 0; Mismatches
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ProDom; PD002381; ATP-sulfurylase; 1.
TIGRFAMs; TIGR00339; sopT; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR002650; ATP-sulfurylase.
                                                                                                                                                                238 NADAVFAFQLRNPVHNGHALLM 259
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                   TIGRFAMS; TIGR00339; SOPT; 1. SEQUENCE 461 AA; 51807 MW;
                                                            Query Match
Best Local Similarity 100...
Rest 22; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     ATP sulfurylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sulfurylase.
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Q42519
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MIN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase (EC 2.7.7.4)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SAMEDLINE-20267847; PubMed-10806350;

RA Hatzfeld Y., Lee S., Lee M., Leustek T., Saito K.;

RA Hatzfeld Y., Lee S., Lee M., Leustek T., Saito K.;

RT sulfurylase isoform from Arabidopsis thaliana.";

RE SELS-58(2000)

RE Gene 248:51-58(2000)

RE MEL; AF198964; AAF19185.1;

DR REME; AF198964; AAF918185.1;

DR Pfam; PF07747; ATP-sulfurylase.

PRODOM; PD002381, ATP-sulfurylase; 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

PRODOM; SOPP: 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

PRODOM; PD02381, ATP-sulfurylase; 1.

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PRODOM; PD02381, ATP-sulfurylase; 1.
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EMBL: X79053; CAA55655.1;
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                                                   Length 463;
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Last annotation update)
(EC_2.7.7.4).
                                             DB 10; L
1.2e-14;
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Pred. No.
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MEDLINE-95004649; PubMed-7920699;
3.68; Sco.
100.08; Pré
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DR Pfam; PF01747; ATP-sulfurylase; 1.

DR ProDom; PD002381; ATP-sulfurylase; 1.

DR TIGREAMS; TIGR00339; sopT; 1.

KW Nucleotidyltransferase; Transferase.

SQ SEQUENCE 463 AA; 51827 WW; 2EGCBC1C1D1263A3 CRC64;

Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy Dp Search completed: May 30, 2003, 12:32:18 Job time : 89 secs

	GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	May 30, 2003, 12:08:55 ; Search time 73 Seconds (without alignments) 1122.591 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-898-165B-7 3271 1 MSGIKKQKTENQQKSTNVVYMAPKAWKVLTDYYRSEMDKN 615
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	908470 segs, 133250620 residues
Total number of	Total number of hits satisfying chosen parameters: 908470
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	3216	;	:	21	AAY79214	Human transferase
7	3162.5			22	AAU32438	Novel human secret
3	2602			19	AAW70494	Human disease rela
4	2602			20	AAY22349	Human APS kinase/A
S	2602			20	AAW67882	Human secreted pro
9	2031.5	62.1	635	22	ABB71650	Drosophila melanod
7	1294			21	AAG44040	Arabidopsis thalia
8	1294			21	AAG44039	Arabidopsis thalia
6	1282.			21	AAG30254	Arabidopsis thalia
10	1282			21		Arabidopsis thalia

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21 AAG30252 AAG09595 AAG09595 22 AAG09595 22 AAG09596 22 AAG4366 23 AAG4366 24 AAG4366 25 AAG4366 21 AAG21121 AAG21122 21 AAG21123 AAY4792 21 AAY4792 22 AAG36409 23 AAY4798 24 AAY4798 25 AAG1477 27 AAG1477 28 AAG1477 28 AAG1477 28 AAG1477 29 AAG1477 21 AAG1477 21 AAG1477 21 AAG1477 21 AAG1477 21 AAG11017 21 AAG11016	AAG383 AAG357 AAG200 AAG145 AAG474
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FISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDS
                                                                                                                                                                    NGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKS
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                                                                                                          AETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLD-----DGVINMS
                                                                                                                                                        296 IPIVLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human transferase proteins useful for preventing, diagnosing and treating cancers and developmental, gastrointestinal, genetic, immunological, neurological, reproductive and smooth muscle disorders
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49..56
/note= "ATP/GTP binding site (P-loop)"
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            "potential O-phosphorylation"
                                    'note= "potential O-phosphorylation"
                                                          "potential O-phosphorylation"
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Pred. No. 2.5e-316;
2; Mismatches 2;
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98US-0186779.
99US-0133642.
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 313
/note=
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439
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Hillman JL, Azimzai Y;
                                                           note=
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Best Local Similarity
Matches 610; Conserv
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04-NOV-1998;
11-MAX-1999;
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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                   Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
Novel human secreted protein #2929.
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2001US-0770160
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61 ALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGEVCITS 120

1 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF 1 MSGIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGACKTISF

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Indels

Conservative

Best Loca Matches

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(first entry)

Human disease related nucleotide kinase-2; DRNK-2; deoxyguanosine kinase;

Human disease related nucleotide kinase-2 (DRNK-2) protein sequence

(first entry)

29-DEC-1998

AAW70494;

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         The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used the increase stem cell proliferation; to regulate hemantopoissis; and in
                                                                                                                                                                                                                                                                                                                                                                               GKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPP
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                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                    bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; a in treatment of leukaemias AMO2510-AAU33304 represent the amino aci sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                         22; Length 648;
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Pred. No. 7.1e-311;
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llarity 97.3%;
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AA.

AAW70494 standard; Protein; 624

RESULT 3 AAW70494 ID AAW7

library (LUNGOOT 12). The DNRR-2 DNR sequence is useful for the production of the corresponding recombinant enzyme. The invention of the corresponding recombinant enzyme. The invention provides DNR enzymes, which are deoxyguanosine kinases, which catalyse the transfer of a terminal phosphate from adenosine triphosphate (ATP) or quanion triphosphate (GTP) to quanosine or quanidine in the requilation of cellular levels of GTP and its corresponding nucleoside triphosphate. As GTP levels are known to control the activity of certain oncogenic proteins e.g. p21ras, a protein involved in cell proliferation and concogenesis, suppression of the enzyme activity causes high ratios of GTP:GDP, promoting oncogenesis. Therefore, diseases (e.g. cancers, immune disorders and neurological dysfunction) related to this lack of activity may be prevented or treated with the recombinant enzyme, or by gene therapy based strategies. Anti-sense constructs of the DNKR encoding nucleic acids may also be used for inhibition of over-expression The present sequence represents a human disease related nucleotide kinase-2 (DRNK-2) protein sequence. The DNKR-2 encoding DNA sequence was first identified in Incyte Clone 373887 from the lung tissue CDNA þ Nucleic acids encoding de:oxy:guanosine kinase - useful for recombinant production of the enzyme for treating diseases caused lack of the enzyme e.g. cancers caused through loss of enzyme "adenosine 3'-phosphate 5'-phosphosulfate (PAPS)-dependent enzyme motif" Hillman JL; Length 624; p21ras; cell proliferation; oncogenesis; cancer; PAPS; immune disorder; neurological dysfunction; gene therapy; adenosine 3'-phosphate 5'-phosphosulfate-dependent enzyme ATP pyrophosphatase PP-motif. "ATP/GTP binding site (p-loop)" "ATP pyrophosphatase PP-motif" Score 2602; DB 19; Pred. No. 4.2e-254; Hawkins PR, 'note= "N-glycosylated" "N-glycosylated" Jocation/Qualifiers Guegler KJ, Examples; Fig 2A-2G; 53pp; English. 79.5%; 77.1%; 97US-0879561 97US-0879561 PHARM INC. 176..187 411..433 /note= /note-/note= /note= Corley NC, 303 WPI; 1998-556388/47 Query Match Best Local Similarity 624 AA; N-PSDB; AAV33482 (INCY-) INCYTE Key Modified-site Modified-site the enzyme 20-JUN-1997; 20-JUN-1997; Homo sapiens US5817482-A 06-0CT-1998 Bandman O, Sequence function Domain Region Region 

Gaps

9 624;

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TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI 178
                                                                                                                                                                                                                                                                                                                 DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR 238
                                                                                                                                                                                                                                                                                                                                                                   VLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAP 598
                                                                                                                                                                                                               KKVKLSNNAQNWGMQRATNVTYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTV
                                                                                                                                                                                                                                                                                     AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
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                                                                                                                                                                                                                                   SFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                      VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH
                                                                                      This sequence is the human-derived APS kinase/ATP sulphurylase of the invention. The enzyme may be used to prepare 3'-phosphoadenosine 5'-phosphosulphate (PAPS) on a large scale.
                              New human-derived APS kinase/ATP sulfurylase gene - useful for large scale preparation of 3'-phosphoadenosine 5'-phosphosulfate
                                                                                                                                                    Length
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein encoded by gene 76 clone HOSFD58
                                                                                                                                                   Score 2602; DB 20;
Pred. No. 4.2e-254;
7; Mismatches 67;
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                                                                     Claim 1; Page 6~7; 9pp; Japanese.
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77.18;
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KAWTVLTEYYKS 620
  WPI; 1999-451549/38,
N-PSDB; AAX84897.
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97US-0048069
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                                                                                                                                                                                                                               WPI; 1999-070066/06.
N-PSDB; AAX00686.
                                                        Misc-difference
                                            Homo sapiens
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30-MAY-1997
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Greene JM,
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ABB71650 standard; Protein; 635 AA.
(see AAX00611 for described uses).
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Protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX0611-X00724; amino acid sequences AAX0611-X00724; amino acid sequences AAX0611-X00724; amino acid sequences AAX06107-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in
               Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Ni J, Olse
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Hu JS, Lafleur DW, Moore PA,
Ruben SM, Shi Y, Young P;
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479 AIFPSPMLYAGPTEVOWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM 538
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                                                                                                                                                                                                                                                                                                                              ALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV
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                                                                                                                                                    9 KKVKLSNNAQNWGMQRATNVTYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTV
                                                                                                                                                                                                   SFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCI
                                                                                                                                                                                                                                                                                                       119 TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH
                                                                                                     KKOKTEN-----QQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTI
                                                    Gaps
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  Length 625;
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                                                 67;
79.5%; Score 2602; DB 20; 77.1%; Pred. No. 4.2e-254; ive 67; Mismatches 67;
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562 GLDSMEILPFRVAAYDKSASRMAFFEPKRKDEFEFISGTKMRTLAKTGASPPDGFMEPEA 621
                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                       AAG44040 standard; Protein; 460 AA
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                                                                                                                                                                                                                                                                                                 termination sequence
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                             601 WKVLTDYYRS
                                                           622 WRILATYYON
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16-JUN-1999
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                                                                                                        RESULT 7
                                                                                                                         AAG44040
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                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPERVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 KTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIH---ELFVPEN-KLDHVRAEAETLPSLS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 NTHGYTVRESTOKLVTLLEQEGIIPRS-LRDVDLLPELYPSESIATEALRHEAESLQAIE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 ITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLD--DGVI--NMSIPIVLPVSA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGD 364
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                                                                                                                                                                                                                                                                                                                                                    sequences (ABLO1840-ABL16175) and the encoded proteins (AABS737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                    detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                             Disclosure; SEQ ID NO 41742; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%; Score 2031.5; DB 22; Lengt
63.4%; Pred. No. 2.8e-196;
ive 94; Mismatches 116; Indels
                                                                                        Myers EW;
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           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and interactions
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Matches. 387; Conservative
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                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL15753.
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01 - JUN - 1999;
03 - JUN - 1999;
04 - JUN - 1999;
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177 ARTWGTTAPGLPYVDEAITNAGNWLIGGDLEVLEPVKYNDGLDRFRLSPAELRKELEKRN 236
                                                                      402 ADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQ 461
                                                                                  HAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPE 521
                                                                                                                                                        522 TKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRM 581
                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                               SRVWGTTCTKHPHI-KMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMN
                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 55115.
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99US-0157865.
99US-0158029.
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99US-0161404.
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99US-0161406.
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99US-0147204
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99US-0147260
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        02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
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1-0CT-1999;
1-0CT-1999;
2-0CT-1999;
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12-AUG-1
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13-AUG-1
16-AUG-1
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26-AUG-1
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18-AUG-1
20-AUG-1
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342
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                                                                                                                                                                                                                                                                             343 SRVWGTTCTKHPHI-KMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMN
                                                                                                                   226 ELFVPENKLDHVRAEAETLPSLSITKLDLQWYQYLSEGWATPLKGFMREKEYLQVMHFDT
                                                                                                                                                           286 L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFVLAHG-GRRVAILRDAEFYEHRKEERC
                                                                                                                                                                                                                                        402 ADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQ
                                                                                                 Gaps
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                                                                              Length
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                                                                            39.6%; Score 1294; DB 21;
ilarity 62.2%; Pred. No. 8.9e-122;
Conservative 61; Mismatches 82;
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          99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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9905-0123548-
9905-0125788-
9905-0125788-
9905-0126785-
9905-0126785-
9905-0128784-
9905-0128714-
9905-0128714-
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  99US-0161359
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                                                                                        Similarity
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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05-MAR-1999;
09-MAR-1999;
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25-MAR-1999;
29-MAR-1999;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
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Best Local Simi.
Matches 242;
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,	9US-01	90S-01	90S-013	9115-019	90S-013	9US-013	9US-013	90S-013	9US-013	9US-013	90S-013	9US-013	990S-013 990S-013	90S-013	9US-013	90S-013	9US-013	90S-013	911S-013	9us-013	9US-013	9US-013	9US-013	9US-013	90S-013	9US-013	9US-013	90S-013	9US-013	9US-013	908-013 908-013	9US-013	9US-013	90S-013 90S-013	9US-013	9US-013	9US-013	9US-013	908-013	9US-014	9US-014	9US-014	9US-014	9US-014 9US-014	9US-014	9US-014	90S-014 90S-014	90S-014	9US-014	90S-014 90S-014	9US-014	9US-014	9US-014	9US-014	9US-014	9US-014
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PR 20-70L-1999; 990S-0144335.
PR 20-70L-1999; 990S-0144632.
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PR 21-70L-1999; 990S-0144632.
PR 21-70L-1999; 990S-0144631.
PR 21-70L-1999; 990S-014568.
PR 22-70L-1999; 990S-014568.
PR 22-70L-1999; 990S-014568.
PR 22-70L-1999; 990S-014568.
PR 23-70L-1999; 990S-0146319.
PR 25-70C-1999; 990S-0151318.
PR 25-70C-1999; 990S-0155139.
PR 25-70C-1999; 990S-01

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99US-0134218
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99US-0135124
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99US-0139763
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28-APR-1999;
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                                        25-FEB-2000;
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05-MAR-1999;
09-MAR-1999;
                         06-SEP-2000
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05-MAY-1999;
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14-MAY-1999;
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   341
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                                                                                                                                                                                                                                                             286 L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFV--LAHGGRRVAILRDAEFYEHRKEER
                                                                                                                                                                                                                 Gaps
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9
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                                                                                                                                                                                                39.2%; Score 1282; DB 21;
62.3%; Pred. No. 1.5e-120;
ive 60; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAG30253 standard; Protein; 465 AA
990S-0159330.
990S-0159331.
990S-0159637.
990S-0159638.
                                     990S-0160741.
990S-0160767.
990S-0160768.
990S-0160700.
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99US-0161993.
99US-0162142.
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                                                                                                                                                                                               Query Match 39.29
Best Local Similarity 62.39
Matches 243; Conservative
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26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
                      14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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21-OCT-19
22-OCT-19
22-OCT-19
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21-0CT-19
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25-0CT-1
25-0CT-1
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226 ELFVPENKLDHVRAEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 QHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521 ETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.2%; Score 1282; DB 21; 62.3%; Pred. No. 1.5e-120;
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 99US-0154039.
99US-0154779.
99US-0155139.
99US-0155686.
99US-0155659.
                                                                  99US-0156596
                                                                                                  99US-0157865
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 16.SEP-1999;
20.SEP-1999;
23.SEP-1999;
24.SEP-1999;
28.SEP-1999;
04.OCT-1999;
05.OCT-1999;
06.OCT-1999;
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3-0CT-1999;
3-0CT-1999;
4-0CT-1999;
1-0CT-1999;
1-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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99US-0143542.
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99US-0144352
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99US-0145085
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99US-0145276
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Gaps

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Length 465; Indels

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99US-0139457.
99US-0139458.
99US-0139460.
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99US-0142154.
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99US-0140354.
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990S-0143624.
990S-0144005.
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990S-0144325.
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99US-014
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18 - JUN - 1999;
22 - JUN - 1999;
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01-JUL-1999;
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29-JUN-1999;
30-JUN-1999;
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 36134.
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990S-0134941.
990S-0135124.
990S-0135629.
990S-0136621.
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99US-0128714.
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990S-0130449.
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990S-0132863.
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99US-0137222.
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99US-0134370
                                                                                                                       (first entry)
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                           RESULT 11
AAG30252
ID AAG30252
ID AAG30
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AC AAG3C
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345
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                                                                                                                         226 IARTWGTTAPGLPYVEEAITNAGDWLIGGDLEVLEPVKYNDGLDRFRLSPFELRKELEKR 285
                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                286 GADAVFAFQLRNPVHNGHALLMTDTRRRLLEMGYKNPILLLHPLGGFTKADDVPLSWRMK
                                                                             401 NADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMK
                                                                 461 QHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHP
                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 7590.
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                                                                                                                                                                     AAG09595 standard; Protein; 473 AA.
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990S-0123548
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990S-0126785.
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99US-0132407
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990S-0151438.
990S-0151930.
990S-0152363.
990S-0153070.
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99US-0161992.
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99US-0154039.
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990S - 0147038 990S - 0147302 990S - 0147192 990S - 0147193 990S - 0147493 990S - 0147493 990S - 0147493 990S - 0147493 990S - 0148171 990S - 0148171 990S - 0148171 990S - 0148171 990S - 0148172 990S - 0148173 990S - 0148173 990S - 0148173 990S - 0148173 990S - 0148173 990S - 0158184 990S - 0159188 990S - 0159188 990S - 0159188 990S - 015188 990S - 01588 990S - 01588	990S - 015933 0. 990S - 015953 1. 990S - 015963 8. 990S - 015963 8. 990S - 016076 1. 990S - 016077 0. 990S - 0160815 9. 990S - 016098 0. 990S - 0161405 0. 990S - 0161405 0. 990S - 016135 0. 990S - 016135 0. 990S - 016135 0.
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99US-0132048
99US-0132407
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                                                                                                                                                         LQWVQVLSEGWATPLKGFMREKEYLQVMHFDTL-LDDGV-INMSIPIVLPVSAEDKTRLE 311
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                                                                                                                                                                                                               GCSKFV--LAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHI-KMVMESGDWLVG 368
                                                                                                                                                                                                                              LLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYA 488
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                                                                                                                   39 LNLVYKRNLTMQSVSKMTVKSSLIDPDGGELVELIVPETEIGVKRAESETMPKVKLNQID 98
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                                        DB 21;
                                        Score 1272.5; DB 21
Pred. No. 1.4e-119;
                                                                    72; Mismatches
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                                        38.9%;
57.0%;
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99US-0123180.
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                                                                      Matches 243; Conservative
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                                        Query Match
Best Local Similarity
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28-OCT-1999;
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                                                                                                                                                                                          DB 21; Length 476;
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                                                                                                                                                                                        38.9%; Score 1272.5; DB 21 57.0%; Pred. No. 1.4e-119; ive 72; Mismatches 92;
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ESLQEK 466
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26-OCT-1999;
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                        18-0CT-1999;
21-0CT-1999;
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termination sequence
                        Arabidopsis thaliana
                                                                                             25-FEB-2000;
                                             EP1033405-A2
                                                                     06-SEP-2000
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                    415
578 GTRMRKLAREGENPPDGFMAPKAWKVLTDYYRSEMDK
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                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                             Arabidopsis thaliana
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05 - MAR - 1999;
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60.5%; Pred. No. 2.1e-119;
iive 65; Mismatches 86;
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286 L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFVLAHG-GRRVAILRDAEFYEHRKEERC 342 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:12 | 1:11 | 1:12 | 1:11 | 1:11 | 1:12 | 1:11 | 1:11 | 1:12 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1
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9905-0149368.
9905-0149175.
9905-0149426.
9905-0149723.
9905-0149929.
9905-0149929.
9905-0149929.
9905-0150864.
9905-0150866.
9905-0150884.
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990S - 0151930
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99US-0160770.
99US-0160814.
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990S-0146389.
990S-0147038.
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990S-0147192.
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Search completed: May 30, 2003, 12:17:32 Job time : 76 secs IDIASH WHIPTER TO BE SHILL

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
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length: 2000000000
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Perfect score:
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Maximum DB seq
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1263.1
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28 98 3.0 414 4 US-09-134-001C-5377 29 96.5 3.0 2987 2 US-08-970-269A-29 31 96.5 3.0 3959 4 US-09-075-562-39 32 96.5 3.0 3959 4 US-08-970-269A-30 33 94.5 2.9 1365 4 US-09-407-562-30 34 94.5 2.9 1365 4 US-09-376-398A-46 35 94 2.9 521 1 US-08-398-627-8 36 94 2.9 521 1 US-08-398-627-8 37 94 2.9 521 1 US-08-398-627-8 38 94 2.9 521 1 US-08-398-627-8 39 94 2.9 521 1 US-08-398-627-8 40 92.5 2.8 510 4 US-09-557-122A-28 41 92.5 2.8 510 4 US-09-562-666-28 42 92.5 2.8 510 4 US-09-567-162-66 43 92.5 2.8 510 4 US-09-56-66-28 44 92 2.8 1222 4 US-09-004-838-119 45 92 2.8 1222 4 US-09-013-8119	Sequence 5377, Ap	Sequence 29, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 46, Appl	Sequence 18, Appl	Sequence 8, Appli	Sequence 28, Appl	Sequence 28, Appl	Sequence 5, Appli	Sequence 4, Appli	Sequence 119, App	Sequence 42, Appl					
80 00 00 00 00 00 00 00 00 00 00 00 00 0	US-09-134-001C-5377	US-09-407-562-29	US-08-970-269A-30	US-09-407-562-30	US-09-222-938A-46	US-09-376-330-18	US-08-090-523-8	US-08-398-627-8	US-08-406-858-8	PCT-US91-04036-8	PCT-US94-05275-8	US-08-557-122A-28	US-09-262-666-28	US-09-784-316-5	US-08-553-436A-4	US-09-004-838-119	US-09-413-814-42	
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8000108454444400000000000000000000000000	98	96.5	96.5	96.5	94.5	94.5	94	94	94	94	94	92.5	92.5	92.5	92	92	95	
	28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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US-08-879-561-3
Sequence 3, Application US/08879561
Sequence 3, Application US/08879561
Sequence 3, Application US/08879561
Sequence 3, Application US/08879561
SERENTAL INPOWATION:
SETTING TO SEQUENCE 1.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Meil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES NUMBER OF SEQUENCES: 12
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
STATE: CA
COUNTRY: USA
COMPUTER: LBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURREWA APPLICATION DATA:
APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
CLASSIFICATION: A24
PRIOR PERDATION: A24
PRIOR APPLICATION NUMBER:
FILING DATE: Herewith
SPETING DATE: HOWNER: B6,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,740
REGISTRATION NUMBER: 36,740
TELEPHONE: 415-855-055
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DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLMODICRRILERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 2599; DB 2;
Pred. No. 1.3e-268;
66; Mismatches 69;
                  US/08/879,561
                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                            79.5%;
                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: amino acid
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Best Local Similarity 77.0
Matches 471; Conservative
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609 KAWTVLVEYYKS 620
 CURRENT APPLICATION DATA:
                             FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                               Herewith
                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1109676
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                                                                                                                                                                                                                                                                      SFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCI
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                                                                                                                                                                                                                                                    DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR
                                                                                                                                                                                                                                                                                                                 239 AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
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9
Length 624;
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Patent No. 5817482
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Nearl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
 Score 2602; DB 2;
Pred. No. 6.1e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSTEM: DOS
FastSEQ for Windows Version 2.0
                Pred. No. 6.1e
67; Mismatches
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79.58;
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                                 Conservative
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MEDIUM TYPE: Diskett
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OPERATING SYSTEM:
SOFTWARE: FASTSEO
                Similarity
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Query Match
Best Local Simi
Matches 472;
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ERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGP 490
                                                                                                                                                                                                              TEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPF 550
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
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61.4%; Pred. No. 3.2e-127;
Live 60; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/346,408B CURRENT FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09346408B Patent No. 6338966
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 61.43
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        611 EMDKN 615
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US-09-346-408-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 IPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                   APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nail C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.4%; Score 2367; DB 2; 71.4%; Pred. No. 7.7e-244; ive 69; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0325 US
                                                                                                                                                                                                                                                              1: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
                                                                Sequence 10, Application US/08879561
Patent No. 5817482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                        Hillman, Jennifer L
Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.49
Best Local Similarity 71.47
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        Diskette
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APPLICATION NUMBER:
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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CLONE: 705385
                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Palo Alto
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                                                                                                                                                                                                                                                                                                                                  USA
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94304
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Best Local S.
Matches 240
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300 HEMVLEDGVLDPETTVVSIFPSPMHYAGPTEVQWHAKARINAGANFYIVGRDPAGMGHPL 359
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APPLICANT: Allen, Steve
APPLICANT: Anderson, Shawn
APPLICANT: Faloo, Garl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER PILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 12
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                                                                                 582 RKLAREGENPPDGFMAPKAWKVLTDYYRS 610
                                                                                                    Sequence 12, Application US/09346408B Patent No. 6338966 GENERAL INFORMATION:
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US-09-346-408-12
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Best Local Similarity 57.3%;
Matches 242; Conservative 7
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RESULT 6 US-09-346-408-6

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362 EKRDLYDADHGKKVLSMAPGLERLNILPFRVAAYDKTQGKMAFFDPSRPQDFLFISGTKM 421
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                                                                                                   APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Folco, Carl
TTLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
TTLE OF INVENTION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER PILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding.Sulfate Assimilation Proteins
FILE REPERENCE: BB-1167-A
CURRENT PILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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61.7%; Pred. No. 4.8e-126;
iive 59; Mismatches 86;
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                                                                                APPLICANT: Allen, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Glycine max US-09-346-408-6
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                              Patent No. 6338966
GENERAL INFORMATION:
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SEQ ID NO 2
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TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION WUBBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
SOFFWARE: Microsoft Office 97
SEQ ID NO 8
                                                                           51;
                                                 Length 465;
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                                                    DB 4;
                                                37.8%; Score 1237.5; DB 4; 50.3%; Pred. No. 2.6e-123; ive 76; Mismatches 120;
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                                                                          250; Conservative
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APPLICANT: Allen, Steve
                                                              Similarity
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US-09-346-408-8
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TYPE: PRT
ORGANISM:
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APPLICANT: Allen, Steve
APPLICANT: Allen, Shawn
APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
TILE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
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; Pred. No. 4.7e-52;
14; Mismatches 15
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BARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-346-408-2; Sequence 2, Application US/09346408B; Patent No. 6338966
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78.2%;
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502 JAGANFYLVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAY----N 556
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APPLICANT: Railco, Carl
APPLICANT: Railco, Carl
AITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: J12
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557 KAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAPKAWKVL 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b; Score 417; DB 4;
b; Pred. No. 1.1e-36;
14; Mismatches 17;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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. Sequence 10, Application US/09346408B
Patent No. 6338966
GENERAL INFORMATION:
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71.3%;
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APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
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Best Local Similarity
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF THE COURTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4517
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4403
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llarity 29.9%; Pred. No. 1.9e-38;
Conservative 82; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 481;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4517
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Best Local Similarity 44.58
Matches 93; Conservative
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Matches 122; Conserv
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1997-03-07 NUMBER: 60/040,626 1997-03-07 NUMBER: 60/040,334 1997-03-07 NUMBER: 60/040,163 1997-03-07 NUMBER: 60/047,600 1997-05-23 NUMBER: 60/047,615 NUMBER: 60/047,615 NUMBER: 60/047,615 NUMBER: 60/047,615 NUMBER: 60/047,615 NUMBER: 60/047,615 NUMBER: 60/047,615	1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 NUMBER: 60/047, 618 1997-05-23 NUMBER: 60/047, 592 1997-05-23 NUMBER: 60/047, 592 1997-05-23 NUMBER: 60/047, 584 1997-05-23 NUMBER: 60/047, 584 1997-05-23 NUMBER: 60/047, 584 1997-05-23 NUMBER: 60/047, 587 1997-05-23 NUMBER: 60/047, 587 1997-05-23 NUMBER: 60/047, 587 1997-05-23 NUMBER: 60/047, 587 1997-05-23 NUMBER: 60/047, 587 1997-05-23 NUMBER: 60/047, 588 1997-05-23 NUMBER: 60/047, 588 1997-05-23 NUMBER: 60/047, 588 1997-05-23 NUMBER: 60/047, 588 1997-05-23 NUMBER: 60/047, 588	NUMBER: 60 1097-05-2 1097-05-2 1097-05-2 1097-05-2 1097-05-2 1097-05-2 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1 1097-04-1
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EARLIER APPLICATION CONTROL OF CO EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER APPLICATION NUMBER: 60/056,808
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,804
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,814
EARLIER APPLICATION NUMBER: 60/056,814
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,814
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,815
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EARLIER APPLICATION NUMBER: 60/056,815
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/056,815
EARLIER APPLICATION NUMBER: 60/056,917
EARLIER APPLICATION NUMBER: 60/056,917 APPLICATION NUMBER: 60/047,593 FILLING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 PLICATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 1997-08-22 FILING DATE: 1997-08-22 1997-04-11 ILING DATE:

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APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,633
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PPLICATION NUMBER: 60/047,617
ILING DATE: 1997-05-23
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APPLICATION UNBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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CATION NUMBER: 60/047,587
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RPLICATION NUMBER: 60/047,632
                                                                           APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,583
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CATION NUMBER: 60/047,598
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PPLICATION NUMBER: 60/047,613
ILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
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LICATION NUMBER: 60/047,492
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PLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,669
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,671
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                                                          1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen-et-al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
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APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
                                          EARLIER FILING DATE: 1997-04.11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-22
                                                                                                                       APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632
                                                                                                                                                                                                                             APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
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APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
                                      FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
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R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/057,761

R PILING DATE: 1997-08-22

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,595

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R PILING DATE: 1997-05-23 LICATION NUMBER: 60/056,630 ING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILLING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 60/043,578 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,874 APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 60/048,974 APPLICATION NUMBER: 60/047,594 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-05-23 1997-05-23 1997-05-23 FILING DATE: 1997-04-11 1997-08-3 FILING DATE: 1997-05 APPLICATION NUMBER: EARLIER EARLIER EARLIER

Gaps 0 Score 198; DB 4; Length 36; Indels Query Match 6.1%; Score 198; DB 4; L Best Local Similarity 100.0%; Pred. No. 4e-14; Matches 36; Conservative 0; Mismatches 0; 1 YOAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGK 36 20 YQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGK 55 EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-66
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER APPLICATION NUMBER: 60/046,696
EARLIER APPLICATION NUMBER: 60/056,606
EARLIER APPLICATION NUMBER: 60/057,650 R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,881

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,909

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,875

R APPLICATION NUMBER: 60/056,875

R APPLICATION NUMBER: 60/056,862

R R PILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/043,670 R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056,632 R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,664 R FILING DATE: 1997-08-22 APPLICATION DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884 EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05 EARLIER APPLICATION NUMBER: 60/049,610 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 FILING DATE: 1997-05-23 BARLIER F
BARLIER F Д δ

Sequence 3, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: W. Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Methods for Tumor Suppressor Genes, Gene Products and
TITLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/038,760 FILING DATE: 19930325 ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS New York US-08-038-760-3 CITY: N STATE:

FILING DATE: 19 CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 RGONRSARIA--KOLENDTRIIEVLCKEHECNIDEVKNVYFKNFI-PFM----NSLGLVT 195
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Best Local Similarity 18.3%; Pred. No. 0.058;
Matches 139; Conservative 100; Mismatches 224; Indels 296; Gaps
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                 NAME: Poissant, Brian M
RECISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (612) 790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-038-760-3
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Search completed: May 30, 2003; 12:21:02 Job time : 29 secs 4466 4466 44666 466666 46666 4

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; OTHER INFORMATION: Incyte ID No. US20020156263A1 1420940CD1
US-09-974-298-184
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APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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Pred. No. 2.5e-281;
2; Mismatches 2;
US-09-984-245-332

US-09-966-262-332

US-09-984-245-332

US-09-984-245-339

US-09-983-966-262-339

US-09-983-966-262-339

US-09-983-966-362-339

US-09-984-245-338

US-09-984-245-338

US-09-986-262-336

US-09-984-245-338

US-09-984-245-338

US-09-984-245-338

US-09-984-245-338

US-09-984-245-333

US-09-984-245-333

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US-09-984-245-333

US-09-984-245-333

US-09-984-245-333
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
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al Similarity 98.4%
610; Conservative
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 Query Match
Best Local S:
Matches 610)
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Sequence 196, App
Sequence 196, App
Sequence 196, App
Sequence 24, App
Sequence 40, Appl
Sequence 40, Appl
Sequence 45, App
Sequence 45, App
Sequence 635, App
Sequence 96, Appl
Sequence 340, App
Sequence 634, App
Sequence 634, App
Sequence 634, App
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1 MSGIKKQKTENQQKSTNVVY......MAPKAWKVLTDYYRSEMDKN 615
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/ Cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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                  5.1.6
Compugen Ltd
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US-09-741-669-457
US-09-864-761-39981.
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US-09-966-262-196
US-09-983-966-196
US-10-143-090-196
US-10-156-239-40
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US-09-966-265-340
US-09-983-966-340
US-10-143-090-340
US-09-809-391-634
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Copyright (c) 1993 - 2003
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                                                     DR FILING DATE: 1997-05-30
DR APPLICATION NUMBER: US 60/048,355
DR FILING DATE: 1997-05-30
DR FILING DATE: 1997-05-30
DR FILING DATE: 1997-05-30
DR APPLICATION NUMBER: US 60/048,150
DR APPLICATION NUMBER: US 60/048,154
DR FILING DATE: 1997-05-30
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DR FILING DATE: 1997-06-30
DR FILING DATE: 1997-08-05
DR FILING DATE: 1997-08-05
DR FILING DATE: 1997-08-19
DR FILING DATE: 1997-08-19
                                      APPLICATION NUMBER: US 60/048,096
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PRIOR FILING DATE: 1997-05-30
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PRIOR PRILING DATE: 1997-08-19
PRIOR PRILING DATE: 1997-08-19
PRIOR PRILING DATE: 1997-08-10
SEQ ID NO 196
LENGTH 624
                     FILING DATE: 1997-05-30
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US-09-984-245-196
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AETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 196, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/984,245 CURRENT FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: 09/154,707 PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
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PPLICATION NUMBER: US 60/041,277
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/042,344
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APPLICATION NUMBER: US 60/041,276
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PAPLICATION NUMBER: US 60/041,281
APPLICATION NUMBER: US 60/048,094
APPLICATION NUMBER: US 60/048,094
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FILING DATE: 1997-05-30
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RESULT 3
Sequence 196, Application US/09966262
PUBLICATION NO. US20030050461A1
GENERAL IRPORMATION: 0. US20030050461A1
APPLICANT: Young et al.
TIPLE OF INVENTION: 97 10010-01
PRIOR PELICATION NUMBER: US/09/966, 262
CURRENT FILING DATE: 1998-09-17
PRIOR PELICATION NUMBER: US/09/966, 262
CURRENT FILING DATE: 1998-09-17
PRIOR PELICATION NUMBER: US 60/041, 277
PRIOR PELICATION NUMBER: US 60/041, 281
PRIOR PELICATION NUMBER: US 60/041, 281
PRIOR PELICATION NUMBER: US 60/041, 281
PRIOR PELICATION NUMBER: US 60/041, 187
PRIOR P
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118
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                                                                    5 KKOKTEN-----QOKSTNVVYQAHHVSRNKRGOVVGTRGGFRGCTVWLTGLSGAGKTTI
                                                                                     TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI
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                                   Gaps
Length 624;
 79.5%; Score 2602; DB 9; 77.1%; Pred. No. 6.1e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 196, Application US/09983966
Fublication No. US20030060619A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/983,966
CURRENT FILING DATE: 2001-10-29
FRIOR APPLICATION NUMBER: US/09/983,966
CURRENT APPLICATION NUMBER: US/09/983,966
FRIOR APPLICATION NUMBER: US/09/154,707
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-03-19
FRIOR APPLICATION NUMBER: US 60/041,277
FRIOR APPLICATION NUMBER: US 60/041,276
FRIOR APPLICATION NUMBER: US 60/041,276
FRIOR FILING DATE: 1997-03-21
FRIOR APPLICATION NUMBER: US 60/041,281
FRIOR APPLICATION NUMBER: US 60/048,094
FRIOR FILING DATE: 1997-03-21
FRIOR APPLICATION NUMBER: US 60/048,094
                                   Mismatches
                                   67;
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                                   Conservative
                 Similarity
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                                              DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 196, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PS2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER: OF SEQ. ID NOS: 343
SOFTWARE: PATENTIN VEV. 2.0
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609 KAWTVLTEYYKS 620
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US-10-143-090-196
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US-10-143-090-196
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LENGTH: 624
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                               PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/048,135
PRIOR PELICATION NUMBER: US 60/048,135
PRIOR PELICATION NUMBER: US 60/048,187
PRIOR PELICATION NUMBER: US 60/048,187
PRIOR PELICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/048,352
PRIOR PELICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/048,095
PRIOR PELICATION NUMBER: US 60/048,131
PRIOR PELICATION NUMBER: US 60/048,355
PRIOR PELICATION NUMBER: US 60/048,351
PRIOR PELICATION NUMBER: US 60/048,154
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/054,804
PRIOR PELING DATE: 1997-05-30
US 60/048,350
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ORGANISM: Homo sapiens
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OY 419- ALLMODTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKOHAAVLEEGVLDPKSTIV 478    11   1   1   1   1   1   1   1   1	6-239-40 ce 40, Application US/1C ation No. USZ0030036074A LINFORMATION: CANT: Glucksman, Maria CANT: Rapeller-Liberman OF INVENTION: US200 OF INVENTION: Upduti REFERENCE: 35800/247645 NT APPLICATION NUMBER: 09 APPLICATION NUMBER: 09 FILING DATE: 2000-02-29 FILING DATE: 2000-02-29 FILING DATE: 2000-03-15 APPLICATION NUMBER: 60 FILING DATE: 2000-03-15 FILING DATE: 2000-03-14	PRIOR APPLICATION NUMBER: 00/191/90 PRIOR FILING DATE: 2000-03-24 PRIOR APPLICATION NUMBER: 09/808,767 PRIOR APPLICATION NUMBER: 09/808,767 PRIOR PELING DATE: 2001-03-15 PRIOR PELING DATE: 2000-03-24 NUMBER OF SEQ ID NOS: 60 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 162 TYPE: PRT PRES: P	Query Match  Query Match  Query Match  Query Match  Query Match  Query Match  17.5%; Score 571.5; DB 9; Length 162;  Best Local Similarity  At RGCTVWLTGLSGAGKTTISFALEEVLVSHAIPCYSLDGDNVRHGLMRNLGFSPGDREENI 100
419 ALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRWKQHAAVLEEGVLDPKSTIV 478	RESULT 6  US-09-771-161A-244  Sequence 244, Application US/09771161A  Sequence 244, Application US/09771161A  BELEAL INCORMATION: APPLICANT: LEVINE, et al. TILE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFRENCE: 802620-2005.1 FILE PERENCE: 802620-2005.1 FILE PERENCE: 802620-2005.1 FILE PERENCE: 802620-2005.1 FILE PRING DATE: 2001-01-26 PRIOR PLING DATE: 2001-01-26 PRIOR PLING DATE: 2000-11-28 PRIOR PLING DATE: 2000-01-12 PRIOR PLING DATE: 2000-01-15 PRIOR PLING DATE: 2000-04-15 PRIOR FILING DATE: 2000-04-12 SOFTWARE: PATENTION NUMBER: 135619 PRIOR FILING DATE: 2000-04-12 SOFTWARE: PATENTION NUMBER: 135619 FRIOR FILING DATE: 2000-04-12 SOFTWARE: PATENTION NUMBER: 135619 FRIOR FILING DATE: 2000-04-12 FRIOR FILING DATE: 2000-04-12 SOFTWARE: PATENTION NUMBER: 135619 FRIOR FILING DATE: 2000-04-12 FRIOR F	18 Similarity 76.6%; Pred. No. 1.1e-224; 469; Conservative 68; Mismatches 69; Indels 6; Gaps 1; 5 KKQKTENQOKSTNVYQAHHVSRNKRGOVVGTRGGFRGCTVWLTGLSGAGKTTI 58	

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EXON NUCLEIC ACID PROBES USEFUL FO
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1 RGCTVWFTGLSGSGKSTIANALERKLFAQGISVYLLDGDNVRHGLNKDLGFSEEDREENI 60
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                                                 101 RRIAEVAKLFADAGLVCITSFISPFAKDRENARKIH----ESAGLPFFEIFVDAPLNICES
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEI
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS, BY MICROARRAY
                                                                                                                                                                                 APPLICANT: FOISYth, R. Allyn
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
TITLE OF INVENTION: proliferation of E. coli
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50.2%; Pred. No. 5.6e-35;
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CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 457, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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US-09-741-669-457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRIAEVAKLFADAGLVCITSFISPFAKDRENARKIH---ESAGLPFFEIFVDAPLNICES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRVGEVAKLFADAGLIVLTSFISPYRADRDQARELHEDGEEAGLKFIEVFVDTPLEVCEQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
TITLE OF INVENTION: 32613, No. US20030077626a1el Human Transporters
FILE REFERENCE: 35800/249468
CURRENT APPLICATION NUMBER: US/10/199,485
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR PILLING DATE: 2001-02-28
PRIOR PLILNG DATE: 2001-02-28
PRIOR PLILNG DATE: 2000-02-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.5%; Score 571.5; DB 9; Best Local Similarity 67.9%; Pred. No. 1.1e-43; Matches 110; Conservative 17; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Pfam consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Pfam consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 42
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/795,693
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10199485 Publication No. US20030077626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 40, Application US/09795693
                                                                                                                                                  APPLICANT: Glucksmann, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Glucksma
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LENGTH: 162
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APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
                                                                                                                                                                                                                                                                                                                                                                                   55 MSGIKKOKTENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKNNDKF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 IRRIAEVAKLFADAGLVCITSFISPFAKDRENARK--IHESAGLPFFEIFVDAPLNICES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 LORIAFVASELTRAGAAVIASPIAPYEHSRQMARDTILKGGGSNNFFLIHVATPLEYCEK 145
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                                                                                                                                                                                                                                                   Score 323; DB 9;
Pred. No. 3.1e-21;
0; Mismatches 13
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
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CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 20001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020165374A1
GENERAL INFORMATION:
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2001-03-16
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146 HDRRGNYAKARRGEVK 161
                       Prior application data removed
NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 635
                                                                                                                                                                                                                                                   Query Match 9.9%;
Best Local Similarity 83.3%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leach, Martin D. APPLICANT: Mehraban, Fuad, APPLICANT: Conley, Pamela APPLICANT: Law, Debbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 41.9
Matches 57; Conservative
                                                                                                                                                 TYPE: PRT CORGANISM: Homo sapiens US-09-809-391-635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-867-550-96
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                         LENGTH: 174
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEARL = 1.2

OTHER INFORMATION: EXPRESSED IN HEARL SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BE292722.1, EVALUE 4.00e-33
US-09-864-761-39981
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EXPRESSED IN BONE MARROW, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39981
LENGTH: 65
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PELLING NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                            APPLICATION NUMBER: US 60/236,359
FILLING DATE: 2000-09-27
                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00664
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Publication No. US20030049618A1
GENERAL INFORMATION:
                                                                       LING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-2
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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SPFAK 65
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APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
                                                                                                               FILE REFERENCE: P2004P1
CURRENT PELLOR NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US 09/154,707
                                                                                                                                                                              APPLICATION NUMBER: US 09/154,707
FILING DATE: 1998-09-17
APPLICATION NUMBER: PCT/US98/05311
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,281
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/048,094
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ION NUMBER: US 60/048,188
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PPLICATION NUMBER: US 60/048,099
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,352
                                                                                                                                                                                                                                              FILING DATE: 1998-03-19
APPLICATION NUMBER: US 60/041,277
                                                                                                                                                                                                                                                                                  FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/042,344
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PLICATION NUMBER: US 60/048,135
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LICATION NUMBER: US 60/048,187
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PELICATION NUMBER: US 60/048,069
LING DATE: 1997-05-30
PLICATION NUMBER: US 60/048,095
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,355
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APPLICATION NUMBER: US 60/048,154
FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/060,862
FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us 60/050,937
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APPLICATION NUMBER: US 60/048,131
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APPLICATION NUMBER: US 60/048,351
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LENGTH: 41
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Pred. No. 1.2e-12;
3; Mismatches 1.
APPLICATION NUMBER: US/09/984,245
                                                                                 APPLICATION NUMBER: PCT/US98/05311
FILING DATE: 1998-03-19
                                                                                                      PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
                                                                                                                                                                                   FILLING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,276
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ION NUMBER: US 60/041,281
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PLICATION NUMBER: US 60/048,188
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CATION NUMBER: US 60/048,099
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LICATION NUMBER: US 60/048,352
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LICATION NUMBER: US 60/048,069
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LICATION NUMBER: US 60/048,095
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APPLICATION NUMBER: US 60/048,094
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PLICATION NUMBER: US 60/048,187
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LICATION NUMBER: US 60/048,131
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Best Local Similarity 90.2
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER:
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US-09-984-245-340
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Length 41; Score 217; Pred. No. 1 6.6%; ilarity 90.2%; Conservative Query Match Best Local Similarity Matches 37; Conserv ORGANISM: HOMO US-09-966-262-340

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Gaps

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Indels

486 LYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDL 526 

ò g RESULT 15 US-09-966-262-340

486 LYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDL 526

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Thu Jun 5 08:31:29 2003

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Search completed: May 30, 2003, 12:28:53 Job time : 49 secs

5 08:31:30 2003

Thu Jun

1

GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM protein - protein search, using sw model  Run on:  May 30, 2003, 12:15:39; Search time 43 Seconds  (without alignments) 1374.946 Million cell updates/sec  Title:  US-09-898-165B-7  Sequence: 1 MSGIKKOKTENOOKSTNVVYMAPKAWKVLTDYYRSEMDKN 615  Scoring table: BLOSUM62  Gapop 10.0, Gapext 0.5  Searched: 283224 seqs, 96134422 residues  Total number of hits satisfying chosen parameters: 283224  Minimum DB seq length: 0  Maximum Match 0%  Maximum Match 0%  Listing first 45 summaries  Database: PPIR_73:* 2: pirst:* 2: pirst:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	-sulfate	adenyly1-sulfate k	3'-phosphoadenosin	sulfate adenylyltr		fate	sulfate adenylyltr	(1)		sulfate adenylyltr	probable sulfate a	adenylylsulfate ki	adenylylsulfate ki	adenylyl-sulfate k	adenylylsulfate ki	adenyly1-sulfate k	adenyly1-sulfate k	adenylylsulfate ki	adenosine 5-phosph	hypothetical prote	1.f	adenosine 5'-phosp	adenosine 5'-phosp		adenylyl-sulfate k	S	->-	LO.	adenylyl-sulfate k	
SUMMARIES	QI	JW0087	JC4383	T24918	S44079	E71409	S44267	544943	T14475	T52659	T01204	T08594	T50101	E96912	S17244	A69839	T06100	AF0408	A83836	AH0856	A87433	B65056	.D91079	E85924 .	S47640	T08076	F82062	B70772	C69877	AD3471	
	h DB													0																	
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dР	Query	79.5	2	7	9.	9.	8.	8	æ	8	7.	۲.	7	16.9	ę.	5	ъ.	5.	4	4	•	4	4.	14.6	4	14.4	4	4	ω,	æ.	
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	Result No.	H	7	m	4	S	9	7	80	6	10	11	. 12	13	14		. 16	17	18	19	20	21	22	23	24	25	26	27	28	29	

probable adenylyl- adenylyl-sulfate k	adenylyl-sulfate k	adenylyl-sulfate k	adenylylsultate ki	ATP sulfurylase, l	probable adenylyl-	adenylyl-sulfate k	adenosine 5'-phosp	sulfate adenylyltr	adenylyl-sulfate k	sulfate adenylyltr	adenylyl-sulfate k	sulfate adenylyltr	sulfate adenylyltr	sulfate adenylyltr
H95932 ZZZRNQ	E95320	H84978	A84073	G82672	C70393	139755	H83472	D75594	S74917	G83835	S18729	S55034	B84073	A53651
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633 2 641 1	7	206 2	208 2	660 2	546 1	620 1	196 2	387 2	177 1	381 2	214 1	574 1	379 2	573 1
13.4 633 2 13.3 641 1	641 2													
	13.3 641 2	13.3	13.1	13.0	12.8	12.7	12.4	12.2	12.1	11.9	11.7	11.4	11.3	11.3

	3.34 3.54	434.3 429 425	13.1	208 208 660	1010	A84073 aden G82672 ATP	adenylylsulfate ki adenylylsulfate ki ATP sulfurylase, l
	36	418	П.П	546 620			oable adenylyl- ovlyl-sulfate k
	38	407		196	7 7		osine 5'-phosp
	40	396	,-,,	177			ylyl-sulfate k
	42	388		381 214	7 7		ate adenylyltr ylyl-sulfate k
	43	374		574	<del>, ,</del> ,		ate adenylyltr
	4 4 4 5	368		573	7 [		ate adenylyltr ate adenylyltr
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	N, Alteri	nate nam ins: ade	nes: ader	nosine Ifate k	5'-	N.Alternar names: adenosine 5'-phosphosulfate kinase; PAPS N.Contains: adenvivisulfate kinase (EC 2.7.1.25); sulfate adenov	ase; PAPS sulfate adenylyltransferase (EC 2-7
	C; Specie	es: Homc	sapien: -1999 #se	s (man)	- re	vision 23-Apr-1999 #text change	
	C; Acces	sion: Jw	40087				
	R; Yanag. Biosci.	isawa, k Biotech	K.; Sakal nnol. Bio	kibara, ochem.	¥.	<u> </u>	ıma, T.; Nakajima, H.
	A; Title	: CDNA C	cloning,	expres	ssto		the human bifunctional ATP
	A; Acces:	sion: JA	10087	*	101	7470406: TIMA (04071506:	•
	A; Moleci	ule type	e: mRNA	,			
	A; Cross	referer	ces: GB	: AF033C	,26;	29.1	; PID:93378101
	A; Exper	imental	source:	Brain			1
	A; Descr	iption:	as aden	ylylsul	fat	e kinase catalyzes the phosphorylation	rylation of adenylylsal
	C; Funct.	ion: <s <="" td=""><td>ATE&gt; as sulfa</td><td>ate ade</td><td>V U.</td><td>ď</td><td>sulfate and</td></s>	ATE> as sulfa	ate ade	V U.	ď	sulfate and
	C; Super	family:	animal	3'-phos	pho	adenosine-5'-phosphosulfate syn	13
	C; Keywo. F; 52-21	rds: mul 5/Domair	ltifunct n: adeny	ional e lylsulf	ate	Keywords: multifunctional enzyme; nucleotide binding; nucleot 52-215/Domain: adenylylsulfate kinase homology <ask></ask>	; nucleotidyltransferase; P-100
	F; 59-66, F; 226-6.	/Region: 20/Domai	nucleo in: sulfa	tide-bi ate ade	indi enyl	ng motif A (P-loop) yltransferase homology <sat></sat>	
	F;133/B	inding s	site: ph	osphate	S) (S	er) (covalent) #status predicted	pa
	Query Best Match	Query Match Best Local Si Matches 472;	ery Match st Local Similarity tches 472; Conserv	79.5%; y 77.1%; rvative 6	1.5%;	Score 2602; DB 1; Length 624 Pred. No. 6.4e-186; 67; Mismatches 67; Indels	24; 6; Gaps 1;
_	Qy	rv ×	KKQKTEN	30	KST	QQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTI	LTGLSGAGKTTI 58
	qa	<b>о</b>	II     KKVKLSNN	- AQNWGMC	::  }RAT		
	ΛO		SFALEEYL	VSHAIPC	XSI	DGDNVRHGLNRNLGFSPGDREENIRRIAEVA	118
	;		MALERYL	I I III		SMALEPYLVCHGIDOVILDGDNIRDGINKNIGEORDREENVBRIAEVAKIEAAAGIVCT	
•	3 (			,	-		0 0
	ΟŊ	d)	rsfispfa. 	KDRENA!	KKIE.	TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI        : :      :	ARAGEIKGFTGI 178
	qq	129 T	FSFISPYT	QDRNNAF	ROIH	EGASLPFFEVFVDAPLHVCEQRDVKGLYKKA	188
	Qy	179 נ	SDYEKPE	TPERVLE	TNI.	DSDYEKPETPERVLKINLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR	JEVPENKLDHVR 238
	qq	189	SEYEKPE	APELVLE	TDS	CDVNDCVQQVVELLQERDIVPVDASYEVKEL	YVPENKLHLAK 248
	Qy	239 ₽	AEAETLPS	LSITKLE	NOT	VOVLSEGWATPLKGFMREKEYLQVMHFDTLL	DDGVINMSIPI 298
	Db	249 T	:    :  DAETLPA	:  LKINKVI	- : -	:     :      : :      :	DGGVINLSVPI 308
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Spescription: as adenylylsulfate kinase catalyzes the phosphorylation of adenylylsul C; Function: <SATF>
C; Function: <SATF>
C; Function: as sulfate adenylyltransferase catalyzes the reaction of sulfate and A b.Description: as sulfate adenylyltransferase catalyzes the reaction of sulfate and A C; Superfamily: animal 3'-phosphoadenosine-5'-phosphosulfate synthetase; adenylylsulfac; Keywords: multifunctional enzyme; nucleotide binding; nucleotidyltransferase; P-loo F; 56-719/Pomain: adenylylsulfate kinase homology <ASK>
F; 180-190/Domain: 3'-phosphoadenosine-5'-phosphosulfate binding #status predicted <PAF; 230-647/Domain: sulfate adenylyltransferase homology <SAT>
F; 137/Binding site: phosphâte (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
     186 OLYAGNKSIDECVOEVVSLLOKNGVVPESAVNIVKELFVPESGLEHAKAEIVDLPTMEIT 245
                                                                              RVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAPKAWKVLTDYYRS 610
                                                                                                                                                                                                                                                                 LQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHALLMQDTCRRLL 430
                                                                                                                                                                                                                                                                                                                                                                  ERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 FALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA93098.1; GSPDB:GN00022; CESP:T14G10.1
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                                                      KLDLOWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPIVLPVSAEDKTRL
                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 19-Jan-2001
                                                                                                                                                               EGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGDWLVGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEVQWHCRSRMIAGANFY IVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSGIKKQKTEN-QQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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Pred. No. 1.4e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'-phosphoadenosine-5'-phosphosulfate synthetase -
N;Alternate names: protein T14G10.1
C;Sports: Caenorhabditis elegans
Grafte: 22-Oct.1999 #sequence_revision 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: CESP:T14G10.1
A,Map position: 4
A;Introns: 23/3; 82/3; 176/1; 535/2; 623/2
C,Function: <ASKF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z68880; PII
A;Experimental source: clone T14G10
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Best Local Similarity 56.5%;
Matches 362; Consedvative 10
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C. Accession: JG3813
R. Rosenthal, E.; Leustek, T.
Gene 165, 243-248, 1995
A. Title: A multifunctional Urechis caupo protein, PAPS synthetase, has both ATP sulfuryl A. Reference number: JG4383; MUID:96096529; PMID:8522184
A. Molecule type: mRNA
A. Residues: 1-610 - RROS-A. GENEL39001; NID:9705384; PIDN:AAB00139.1; PID:9705385
A. Cross-references: GB:L39001; NID:9705384; PIDN:AAB00139.1; PID:9705385
C. Genetics: A. Genetic
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                                                                                                                               VLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAEAETLPSLSIT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylyl-sulfate kinase (EC 2.7.1.25) - spoonworm (Urechis caupo)
N;Alternate names: adenosine 5'-phosphosulfate kinase; PAPS
N;Contains: adenylylsulfate kinase (EC 2.7.1.25); sulfate adenylyltransferase
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C.Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 03-Jun-2002
                             VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH
                                                                                                                                                                                                                                                                                                               AIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM
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	DGDNIRHGLCKNLGFSKEDRQENIRRVAEVAK	NARKIHESAGLPFEIFVDAPLNICESRDVKGLYKRAR 	VVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHE	LSITKLDLQWVQVLSBGWATPLKGFMREKEYLQVMHFDT : :  :   :	DGVINMSIPIVLPVSAEDKTRLEGCSKFVLAHGGR 	VWGTTCTKHPHIKMVMESGDMLVGGDLQVLEKIRMNDGL 	VFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHP 	AVLEEGVLDPKSTIVAIPPSPMLYAGPTEVQWHCRSRMIA   :           :   AVIAERVLDPEWTVLSIFPSPMWYAGPTEVQWHARSRIAA	KDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMD                                    DALYETTHGAKVLSMAPGLSALHILPFRVAAYDKTAKKMS	61 65	•	rase (EC 2.7.7.4) met3-1 - potato	guence_revision 10-Nov-1995 #text_change	<pre>k:; Willmitzer, L.; Riesmeler, J.W. 94 characterization of two cDNA clones enco</pre>	7497; MUID:95004649; PMID:7920699	)> IBL:X75041; NID:g471342; PIDN:CAA52953.1;	adenylyltransferase met3-1; sulfate aden itransferase te adenylyltransferase homology <sat></sat>	39.7%; Score 1299; DB 2; Length 42 ( 61.7%; Pred. No. 5.1e-89; evative 64; Mismatches 81; Indels	DHVRAEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMRE 	NMSIPIVLPVSAEDKTRLEGCSKFVL-AHGGRRVAILRDA    :

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A; Residues: 1-476 < KLO>
A; Cross-references: EmBL:X79210; NID:g487403; PIDN:CAA55799.1; PID:g487404
A; Cross-references: EmBL:X79210; NID:g487403; PIDN:CAA55799.1; PID:g487404
B; Murillo, M.; Leustek, T.
Arch. Biochem. Biophys. 323, 195-204, 1995
A; Title: Adenosine-5' - triphosphate-sulfurylase from Arabidopsis thaliana and ine-5' - triphosphate-sulfurylase cDNAs from Arabidopsis thaliana and analysis A; Reference number: S68024; MuID:96019964; PMID:7487067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1.476 (MUW)
A; Residues: 1.476 (MUW)
A; Cross-references: EMBL:U06276; NID:g1228103; PIDN:AAA92351.1; PID:g1228104
A; Experimental source: clone APS2
                                       RESULT 7
84943
sulfate adenylyltransferase (EC 2.7.7.4) met3-1 precursor - Arabidopsis thal
Nylternate names: ATP sulfurylase; sulfate adenylyltransferase APS2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Scession: S44943; S68024; S68202
R;Klonus, D.
submitted to the EMBL Data Library, May 1994
A;Reference number: S44943
A;Reference number: S44943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Klonus, D.; Hoefgen, R.; Willmitzer, L.; Riesmeier, J.W.
Plant J. 6, 105-112, 1994
A;Title: Isolation and characterization of two cDNA clones encoding ATP-sulfurylases fro
A;Reference number: S67497; WUID:95004649; PMID:7920699
A;Accession: S67498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: met3-2
S.Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology
C;Keywords: chloroplast; nucleotidyltransferase
F;50-448/Domain: sulfate adenylyltransferase homology <SAT>
                                                                                                                                                                   520
CSRVWGTTCTKHPHI-KMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEM 400
                                                                                                                                                                                                                                                                          343 SRVWGTTCTKHPHIKM-VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMN 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRM 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato
C;Species: Solanum tuberosum (potato)
C;Date: 08-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S67498; S44267
                                                                                                                                                                                       241 GADAVFAFQLRNPVHNGHALLMTDTRRRLLEMGYKNPILLLHPLGGFTKADDVPLSWRMK
                                                                                                                                                                 QHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHP
                                                                                                                                                                                                                                                  ETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-463 <KLO>
A;Cross-references: EMBL:X79053; NID:g479089; PIDN:CAA55655.1; PID:g479090
                                                                                NADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ELFVPENKLDHVRAEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFVLAHG-GRRVAILRDAEFYEHRKEERC
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                                                                                                                                                                                                                                                                                                                                    MRKLAREGENPPDGFMAPKAWKVLTDYYRS 610
                                                                                                                                                                                                                                                                                                                                                            60; Mismatches
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Best Local Similarity 61.4%
Matches 239; Conservative
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A.Description: EC 2.7.7.4 [validated, MUID:20267847]
A.Pathway: sulfate assimilation
C.Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homclo C.Keywords: chloroplast; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes activation of sulfate to adenylyIsulfate C;Superfamily: sulfate adenylyItransferase met3-1; sulfate adenylyItransferase met3-1; sulfate adenylyItransferase C;Keywords: nucleotidyItransferase F;710-473/Domain: sulfate adenylyItransferase homology <SAT>
A;Title: Functional characterization of a gene encoding a fourth ATP sulfurylase isof
A;Reference number: 226165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-489 <BOL>
A;Cross-references: EMBL:AF016305; NID:g2738749; PIDN:AAB94542.1; PID:g2738750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRVWGTTCTKHPHI-KMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMN 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NiAlternate names: ATP sulfurylase.
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Lo-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: T01204
R;Bolchi, A.; Petrucco, S.; Foroni, C.; Tenca, G.L.; Ottonello, S.
submitted to the RMBL Data Library, July 1997
A;Description: Sulfate permease and ATP sulfurylase mRNA are coordinately mc
A;Reference number: Z14260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 LEVPENKLDHVRAEAETLPS-LSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFVLAHG-GRRVAILRDAEFYEHRKEERC
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                                                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                            Score 1259.5; DB Pred. No. 5.2e-86;
                                              A; Accession: T52659
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                     PIDN: CAB42640.1
                                                                                                                                                                                                                                                                                                                                                                 38.5%; Sco. 60.7%; Pred No. 5.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sulfate adenylyltransferase (EC 2.7.7.4) - maize
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                                                                                     A; Molecule type: mRNA
A; Residues: 1-469 < HAT>
A; Cross-references: EMBL:AJ012586; PIDN:CAB
A; Experimental source: cultivar Columbia
C; Genetics:
A; Gene: aps4
A; Genome: nuclear
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A) Experimental source: cultivar Paulo; C, Function:
                                                                                                                                                                                                                                                                                                                                                                                                                          236; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Description: catalyzes the activation of sulfate to adenylylsulfate Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology Keywords: nucleotidyltransferase
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C;Bate: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
C;Accession: T52659
C;Accession: T52659
C;Accession: Y: Lee, N.; Lee, M.; Leustek, T.; Saito, K.
Gene 248, 51-58, 2000
                                                                         Accession: Target and the EMBL. Devision 20-Sep-1999 #text_change 21-Jan-2000 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000 C; Accession: Tid475
R; Hatzfeld, Y.; Logan, H.M.; Cathala, N.; Davidian, J.C.
Submitted to the EMBL Data Library, September 1996
A; Reference number: Z18111
A; Reference number: Z18111
A; Residues: 1483 * ART>
A; Residues: 1483 * ART>
A; Residues: 1483 * ART>
A; Residues: 1850
A; Trons: 185/2; 407/3; 436/3
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Description: catalyzes the activation of sulfate to adenylylsulfate
C; Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase
F; 68-466/Domain: sulfate adenylyltransferase homology <STR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         (EC 2.7.7.4) ASBo precursor - wild cabbage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.7%; Score 1265; DB 2; Best Local Similarity 50.4%; Pred. No. 2.1e-86; Matches 255; Conservative 79; Mismatches 120;
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                                       sulfate adenylyltransferase (EC 2.7
N;Alternate names: ATP sulfurylase
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68; Score 1230.5; DB 1; Length 489; 18; Pred. No. 8.1e-84; 66; Mismatches 86; Indels 9; ABAETLP-SLSITKLDLOWVQVLSEGWATPLKGFMREK	OY 401 NADAVFAFQLRNPVHNGHALLMODTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMK 460  1
Db 80 DLVAPEEGGRRAALRREAAELPHRLGRVDKEWVHVLSEGWASPLQGFWRDDEFLQTLH 139	
QY 283 FDTLLDDGVINMSIPIVLPVSAEDKTRLEGCSKF-VLAHGGRRVAILRDAEFYEHR 337   :     :	QY 521 ETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKRAMDFYDPARHNEFDFISGTR 580
QY 338 KEERCSRVWGTTCTKHPHI-KNVMESCDWLVGCDLQVLEKIRNNDGLDQYRLTPLELKQK 396      :           : : :                :	Qy 581 MRKLAREGENPPDGFWAPKAWKVLTDYYRS 610 
Qy 397 CKEMNADAVFAPQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLD 456 . 260 FARRNADAVFAFQLRNPVHNGHALLMTDTRKRLLEMGYKNPVLLPHPLGGFTKADDVPLS 319	SULT 12 0101
OY 457 WRWKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAG 516	st (S
QY 517 MPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFI 576	R.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D. submitted to the EMBL Data Library, February 2000 A.Reference number: Z25037 A.Accession: T50101
Qy 577 SGTRMRKLAREGENPPDGFMAPKAWKVLTDYYRS 610  1   1   1   1   1   1   1   1   1   1	A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA A:Residues: 1-202 <woo> A:Across: references: EMBL:AL188056; PIDN:CAB76273.1; GSPDB:GN00066; SPDB:SPAC1782.11 A:Expacimental course: etrain 97294.1</woo>
RESULT 11 T08594	C;Genetics: SPDB:SPAC1782.11
probable sulfate adenylyltransferase (EC 2.7.7.4) - rape C:Species: Brassica napus (rape) C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000	A, introns: 157/1 C;Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
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A; Title: Leaf senescence in Brassica napus: cloning of senescence related genes by subtra A; Reference number: 216446; MUID:97260386; PMID:9106506 A; Accession: T08594 A; Status: preliminary; translated from GB/EMBL/DDBJ	15 STUVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSH :  :
A; Molecule type: mRNA A; Residues: 1-459 <buc> A; Cross-references: EMBL:U68218; NID:g1527218; PIDN:AAB53100.1; PID:g1527219 A; Experimental source: cv. Falcon; senescing leaves</buc>	OY 75 SLDGDNVRHGLMRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENARK 134
C;Genetics: A;Gene: LSC680 C;Function: A;Description: catalyzes the activation of sulfate to adenylylsulfate	QY 135 IHESAGLPFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPERVLKT 194 
C;Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology C;Keywords: nucleotidyltransferase F;48-444/Domain: sulfate adenylyltransferase homology <sat></sat>	195 NLSTVSDCVHQVVELLQEQNIV 216
Query Match 37.1%; Score 1212.5; DB 2; Length 459; Best Local Similarity 59.0%; Pred. No. 1.6e-82; Matches 230; Conservative 63; Mismatches 92; Indels 5; Gaps 5;	DD 1/8 HTQSIEECVEKIVNYLLEKDLI 199 RESULT 13
QY 226 ELFVPENKLDHVRAEAET-LPSLSITKLDLQWVQVLSEGWATPLKGFWREKEYLQVMHFD 284	E96912  E96912  E96912  Chadenylylsulfate kinase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
Oy. 285 TL-LDDG-VINMSIPIVLPVSAEDKTRLEGGSKFVLAHG-GRRVAILRDAEFYEHRKEER 341 1	C;Accession: E90912 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
QY 342 CSRVWGTTCTKHPHI-KMVMESGDMLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEM 400 11	A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A.Reference number: A96900; MUID:21359325; PMID:21359325 A.Accession: E96912 A.Status: preliminary A.Molecule type: DNA

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adenyisurrate Kinasa follolog yisz - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: G:Dec-1997 #sequence_revision 05-Dec-1997 #text_change 19-Jan-2001
C;Accession: A69839
E;Kunst, F; Oqasawara, N; Moszer, I; Albertini, A.M.; Alloni, G:; Azevedo, V.; Ber
R;Kunst, F; Oqasawara, N; Bruschi, C.V.; Caldwell, B.; Capuano, V; Carter, N.M.;
A; Ehrlich, S:D Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari,
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R;eqer, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scal
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sea
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiga
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshila
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtill,
A;Reference number: A69880; Multo: Anderson Anders
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A;Experimental source: strain 168
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                                                                                                                                                                              24 GCTIWLTGLSASGKSTIACALEOLLLOKNLSAYRLDGDNIRFGLNKDLGFSEKDRNENIR
                                                                                                                       42 GCTVWLTGLSGAGKTTISFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIR
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                     Gaps
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                     47; Indels
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Pred. No. 6e-30;
                     Mismatches
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A. Molecule type: DNA
A. Residues: 1-202 < KCRP
A. A. Cross references: GB:855315; NID:9235814; PIDN:AAB19854.1; PID:9235815
B. Duesterhoeft, A.; Philippsen, P. Yeast 8, 749-759, 1992
A. Title: DNA sequencing and analysis of a 24.7 kb segment encompassing centromere CENII
A. Reference number: $25322; MUID:93070612; PMID:1441752
A. Accession: $25323
A. Status: nucleic acid sequence not shown
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: STAIN $288C
A. Cross references: EMBL:X65124; NID:93517; PIDN:CAA46252.1; PID:93529
A. Experimental source: strain $228C
A. Experimental $225C
A. A. Mosecule source between $225C
A. A. Mosecule source $225C
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A. Molecule type: DNA
A. Molecule type: MIPS: VKL001c
A. Cross-references: SCD: Molecule type: MIPS: VKL001c
A. Cross-references: SCD: Molecule type: MIPS: VKL001c
A. Molecule type: MIPS:
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C; Accession: S17244; S25333; S37811
R; Korch, C.; Mountain, H.A.; Bystroem, A.S.
Mol. Gene. Genet. 229, 96-108, 1991
Mol. Gen. Genet. 229, 96-108, 1991
A; Tritle: Cloning, nucleotide sequence, and regulation of MET14, the gene encoding the A; Reference number: S17244; MUID:91375456; PMID:1654509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
A;Cross-references: GB:AE011437; PIDN:AAK78088.1; PID:g15022928; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 IPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 NARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 NQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSHA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenylyl-sulfate kinase (EC 2.7.1.25) - yeast (Saccharomyces cerevisiae)
N;Alternate names: adenosine-5-phosphosulfate kinase; protein YKL001c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology C; Keywords: ATP; P-loop; phosphotransferase; purine nucleotide binding F; 24-187/Domain: adenylylsulfate kinase homology <ASK>F; 31-38/Region: nucleotide-binding motif A (P-loop) F; 37/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                    A;Gene: CAC0103
C;Superfamily: adenylylsulfate kinase; adenylylsulfate kinase homology
                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 202;
                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 551.5; DB 2
51.5%; Pred. No. 8.8e-34;
Live 37; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523; DB 1;
Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 VLKTNLSTVSDCVHQVVELLQEQNIV 216
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56.6%;
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Matches 106, Conservative
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May 30, 2003, 12:08:59 ; Search time 24 Seconds (without alignments) 1062.831 Million cell updates/sec Run on:

US-09-898-165B-7 3271 1 MSGIKKQKTENQQKSTNVVÝ......MAPKAWKVLTDXYRSEMDKN 615 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0?5

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	095340 h bifunctio	088428 m bifunctio	Q60967 m bifunctio		054820 c bifunctio	Q92203 emericella					Q9kct0 bacillus ha		-		Q9kp21 vibrio chol	E		bacillu	r nodq	r nodq			Q9k7h6 bacillus ha	×	ø		Sd	P56864 deinococcus	P78937 schizosacch	P72940 synechocyst	P29811 pseudomonas	-	006736 bacillus su
SUMMARIES	ID	PPS2_HUMAN	PPS2_MOUSE	PPS1_MOUSE	PPS1_HUMAN	PPS1_CAVPO	KAPS_EMENI	KAPS_YEAST	KAPS_PENCH	CYC2_BACSU	KAP2_ARATH	CYC1_BACHD	CYSC_ECOLI	KAP1_ARATH	KAPS_CATRO	CYSC_VIBCH	CYSN_MYCTU	NODQ_RHISB	CYC1_BACSU	NODQ_RHITR	NODQ_RHIS3	NODQ_RHIME	CYSC_BUCAI	CYC2_BACHD	CYSN_XYLFA	SATC_AQUAE	NODQ_AZOBR	CYC1_PSEAE	SAT_DEIRA	MET3_SCHPO	CYSC_SYNY3	CYC2_PSEAE	MET3_EMENI	SAT2_BACSU
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066036 chromatium P74241 synechocyst	P56861 deinococcus Q12650 penicillium	O34764 bacillus su Q9y872 candida alb	Q9ycr6 aeropyrum p P08536 saccharomyc		P56862 approceds	Q9ycr4 aeropyrum p
SAT_CHRVI SAT_SYNY3	CYSC_DEIRA MET3_PENCH	SAT1_BACSU MET3_CANAL	CYSC_AERPE MET3_YEAST	SAT_ENTHI	MET3_ASPTE	SAT_AERPE
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397	192	382	186 521	423	568	389
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34 35	36	3 3 3 3	40 41	42	44	4 5

## ALIGNMENTS

RESULT 1 PPS2_HUMAN PPS2_HUMAN PPS2_HUMAN PPS2_HUMAN PPS2_HUMAN DT 105-30 DT 105-30 DT 105-30 DD E SYDTE DD E CAC 2 DD E CAC 2 DD E CAC 3 DD E
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                                                                                                                                                                                                                                                   Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

L. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

C. I. FUNCTION. BIFUNCTIONAL ENZYME WITH BOTH ATP SULFURYLASE AND APS

KINASE ACTIVITY, WHICH MEDIATES TWO STEPS IN THE SULFATE

GROUP TO AIP TO YIELD ADENOSINE 5'-PHOSPHATE GROUP FROM ATP TO AFE

SECOND STEP IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APS

VIELDING 3'-PHOSPHADADENYLXLSULFATE (PAPS: ACTIVATED SULFATE DONOR USED BY SULFOTRANSFERASE): IN MAMMALS, PAPS IS THE SOLE SOURCE OF SULFATE; APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATE-

C. SULFATE; APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATE-

C. SULFATE, APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATE-

DURING POSTMATAL GROWTH (BY SIMILARITY).

C. I. CATALYTIC ACTIVITY: ATP + adenylylsulfate = Abphosphate + adenylylsulfate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphodenylylsulate.

PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONIES, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIPIDS, DANGS AND XENOBIOTICS.

ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; are produced by alternative splicing.

TISSUE SPECIFICITY: EXPRESSED IN CAPTILAGE.

DISEASE: DEFECTS IN PAPESS ARE THE CAUSE OF SPONDYLOEPIMETAPHYSEAL DISEASE: DEFECTS IN PAPESSED IN CAPTILAGE.

PREMARILY ENDINYSEAL WITH ONLY MILD METAPHYSEAL ABNORMALITIES.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIODUM, FUNCTORY, TITGROUGES; apsK; 1.
TIGRRAMS, TITGROUGES; apsK; 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme;
ATP-binding; Multigene family; Alternative splicing.
NOMAIN 1 ?210
ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE ADENYLYLTRANSFERASE FAMILY.
sulfurylase/adenosine 5'-phosphosulfate kinase isoform SK2.";
J. Biol. Chem. 274:33306-33312(1999).
                                                                           SEQUENCE FROM N.A. (ISOFORM B)...
Venkatachalam K.V., Fuda H., Strott C.A.;
13. Tphosphoadenosine 5'-phosphoaulate synthase 2b isoform.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
Probom; PD002350; APS_kinase; 1.
Probom; PD002350; APS_kinase; 1.
Probom; PD002350; APS_kinase; 1.
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                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A).
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AF160505; AAF40307.2; J
AF160506; AAF40307.2; J
AF160507; AAF40307.2; J
AF173365; AAF12761.1;
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EMBL; BC009894; AAH09894.1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHAL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAI 480
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088428; 092274;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthethase 2 (PAPS synthethase 2) (PAPS 2) (Sulfurylase kinase 2) (SK2) (SK 2)
[Includes: Sulfate ademylytransferase (EC 2.7.7.4) (Sulfate ademylate transferase) (SAP) (AFP-sulfarylase); Ademylylsulfate kinase (EC 2.7.1.25) (Ademylylsulfate 3'-phosphotransferase) (APS kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                   DYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAE
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                                                                                                                                                                                                                                                                  1 MSGIKKOKTENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF
                                                                                                                                                                                                                                                                                                 1 MSGIKKOKTENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISF
                                                                                                                                                                                                                                                                                                                                  61 ALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITS
                                                                                                                                                                                                                                                                                                                                                                                                121 FISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORMS THE PHOSPHOSERINE INTERMEDIATE (B: SIMILARITY).

PP-MOTIFE (BY SIMILARITY).

D -> DGMALP (IN ISOFORM B).

R -> K (IN REF. 2).

E -> G (IN REF. 3).

R -> C (IN REF. 1).

P -> L (IN REF. 1).

P -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                Score 3236.5; DB 1; Length 614;
Pred. No. 1.2e-225;
2; Mismatches 1; Indels 1;
 SULFATE ADENYLYLTRANSFERASE
                   (POTENTIAL)
                                                                                                                                                                 69500 MW;
                                                                                                                                                                                                  98.98;
99.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 Similarity 99.3 611; Conservative
                                                                 515
288
166
361
426
567
                                                                                                                                                                 614 AA;
                                                                               288
166
361
426
567
DOMAIN
NP_BIND
ACT_SITE
                                                                                                              CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                               VARSPLIC
CONFLICT
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Best Local
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                                                                 SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98442651; PubMed-9771708; Ul Haque M.F., King L.M., Cantor R.M., Rusiniak M.E., Swank R.T., Superti-Furga A., Haque S., Abbas H., Ahmad W., Ahmad M., Cohn D.H.; "Mutations in orthologous genes in human spondyloepimetaphyseal dysplasia and the brachymorphic mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0455; apsK; 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme;
ATP-binding; Multigene family; Disease mutation; Polymorphism.
                                                                                                                                                                                                                                                                                                                     Kurima K., Warman M.L., Krishnan S., Domowicz M., Krueger R.C. Jr.,
Deyrup A., Schwartz N.B.;
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                                                                                                                                                                                                                                                    "A member of a new family of sulfate activating enzymes causes brachymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., VARIANT BM ARG-79, AND VARIANT LYS-109.
STRAIN=PWK; TISSUE=Spleen;
(Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-phosphoadenosine-5'-phosphosulfate synthetase)].
PAPSS2 OR ATPSK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:8681-8685(1998).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT BM ARG-79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
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Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                       MEDLINE=98337975; PubMed=9671738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002350; APS_kinase; 1.
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                                                                                            Mus musculus (Mouse).
                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                            TISSUE=Liver;
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MESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHA 419
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2000 (Rel. 39, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                      6 KMNHKRDQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KKOKTENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEE
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                                                                FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                        PP-MOTIF (BY SIMILARITY).

G -> R (IN BM; ACTIVITY ABOLISHED)

R -> K.

S -> F (IN REF. 2).

MISSING (IN REF. 2).

DE375F06A79EFAAB CRC64;
                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                       DB 1; Length
ADENYLYLSULFATE KINASE.
SULFATE ADENYLYLTRANSFERASE.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    26; Indels
                                                                                                                                                                                                                                                                     Score 2985.5; DB ]
Pred. No. 1.5e-207;
; Mismatches 26;
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                                                                                          SIMILARITY).
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92.0%;
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AWKVLTDYYRS
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621 AA;
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124
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Q60967;
                                             NP_BIND
ACT_SITE
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CONFLICT
CONFLICT
SEQUENCE
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Best Local
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VARIANT
  DOMAIN
                       DOMAIN
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                                                                                                                                                                                                                   "The isolation and characterization of cDNA encoding the mouse bifunctional ATP sulfurylase-adenosine 5'-phosphosulfate kinase."; J. Biol. Chem. 270:29453-29459(1995).

FUNCTION: BIFUNCTIONAL ENZYME WITH BOTH ATP SULFURYLASE AND APS KINASE ACTIVITY, WHICH MEDIATES TWO STEPS IN THE SULFATE ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULFATE GROUP TO ATP TO YIELD ADENOSINE 5'-PHOSPHATE GROUP FROM ATP TO APS SECOND STEP IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APS VIELDING 3'-PHOSPHADENYLYLSULFATE (PAPS: ACTIVATED SULFATE DONOR SULFATE; APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SULFATE ACTIVATION PATHWAY. ALSO INVOLVED IN THE BIOSYNTHESIS OF SULFATED ASSELBCTION ACTIVATION PATHWAY. ALSO INVOLVED IN THE BIOSYNTHESIS OF SULFATED ASSELBCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CATALYTIC ACTIVITY: ATP + SULfate = diphosphate + adenylylsulfate.
-1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
phosphoadenylylsulfate.
-1- PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYMTHESTS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIPIDS, DRGGS AND XENOBIOTICS.
-1- TISSUE SPECIFICITY: EXPRESSED IN THE NEONATAL BRAIN AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                        Li H., Deyrup A., Mensch J.R. Jr., Domowicz M., Konstantinidis A.K.,
Schwartz N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotidyltransferase; Kinase; Multifunctional enzyme;
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
9
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(Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADENYLYLSULFATE KINASE.
SULFATE ADENYLYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B487EFAF9B78BE3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                 phosphoadenosine-5'-phosphosulfate synthetase)]
PAPSSI OR PAPSS OR ASAPK OR ATPSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODING MOISTAGEST, PAPSSI.
INTERPRO: IPR002891, APS. Kinase.
InterPro: IPR002650, ATP-sulfurylase.
Pfam: PP01783, APS. Kinase, 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
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                                                                                                                                                                        MEDLINE-96094345; Pubmed-7493984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADENYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70794 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U34883; AAC52328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIGREAMS; TIGRO0455; apsK; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.09
Matches 471; Conservative
                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 AA;
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
ATP-binding;
                                                                                                                                                      TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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5 KKQKTEN-----QQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTI 58

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68

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VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLIMODICRRILLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAP 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPSI_HUMAN STANDARD; PRT; 624 AA.

PO31252; 043841; 075332;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotations (S. 7-7, 4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylylsulfate adenylate (CC 2-7.1.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase)
17-JUN-2002 (AADPSH)
18-JUN-2002 (AADPSH)
19-JUN-2002 (AADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 TDAEALPALKINKVDMQWVQVLAEGWATPLNGFMREREYLQCLHFDCLLDGGVINLSVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFALEEY LVSHA I PCYSLDGDNVRHGLNRNLGFSPGDREEN I RRI A EVAKLFADAGLVCI
                                      TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGI
                                                                                                                                                                                     DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Girard J.-P., Baekkevold E.S., Amalric F.; "Sulfation in high endothellalvenules: cloning and expression of the human PAPS synthetase."; FASEB J. 12:603-612(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98236023; PubMed=9576487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=98334672; Pubmed=9668121;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIFIDIS, DRUGS AND XENOBLOTICS.

TISSUE SPECIFICITY: EXPRESSED IN TESTIS, PANCREAS, KIDNEY, THYMUS, PROSTATE, OVARY, SMALL INTESTINE, COLON, LEUKOCYTES AND LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE ACTIVITY, WHICH MEDIATES TWO STEPS IN THE SULFATE
ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULFATE
SECOND TO APP TO VIELD ADENOSINE 5'-PHOSPHOSULFATE (APS), AND THE
SECOND STEP IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APS
YIELDING 3'-PHOSPHOADENYLYLGSULFATE (PAPS: ACTIVATED SULFATE DONOR
USED BY SULFOTRANSFERASE). IN MAMMALS, PAPS IS THE SOLE SOURCE OF
SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PATHWAY. ALSO INVOLVED IN THE BIOSYNTHESIS OF SULFATED LASEACTIVITION LIGAMOS IN ENDOPHRALIAL CELLS.

LASTALYTIC ACTIVITY: APP + sulfate = diphosphate + adenylylsulfate CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD002350; APS_Ainase; 1.
Probom; PD002381; ATP-sulfurylase; 1.
TIGRAMs; TIGR00455; apsk; 1.
Transferase; Nucleotidyltransferase; Kinase; Multifunctional enzyme; ATP-binding; Multigene family.
Venkatachalam K.V., Akita H., Strott C.A.; "Molecular cloning, expression, and characterization of human bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: BIFUNCTIONAL ENZYME WITH BOTH ATP SULFURYLASE AND APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS OF HIS-151; ASN-426; GLY-427 AND HIS-428.
MEDLINE-99115594; PubMed=9915785; VARALCARD-99115594; PubMed=9915785; VARALCARD-99115594; PubMed=9915785; VARALCARD-99115594; PubMed H., Koonin E.V., Strott C.A.; SIte selected mutagenesis of a conserved nucleotide binding HXGH motif located in the ATP sulfurylase domain of human bifunctional 3, Phosphoadenosine 5, Phosphoauliate synthase."; J. Biol. Chem. 274:2601-2604(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSO EXPRESSED IN HIGH ENDOTHELIAL VENULES (HEV) CELLS AND IN
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                                                                                                                                                                                                                                                                                                                      Yanagisawa K., Sakakibara Y., Suiko M., Takami Y., Nakayama T., Nakajima H., Takayanagi K., Natori Y., Liu M.-C., "cDNA cloning, expression, and characterization of the human bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADENYLYLSULFATE KINASE.
SULFATE ADENYLYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iosci. Biotechnol. Biochem. 62:1037-1040(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoadenylylsulfate.
ENZYME REGULATION: INHIBITED BY CHLORATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; APP-Sulfurylase.
Pfam; PP01583; APS_kinase; 1.
Pfam; PP01747; ATP-sulfurylase; 1.
                                                                                                                                                 Biol. Chem. 273:19311-19320(1998).
                                                                                                                                                                                                                                                                                        MEDLINE=98312048; PubMed=9648242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y10387; CAA71413.1; -.
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                                                                                                                domains
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                              rISSUE=Brain;
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                                                                                                                    functional
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           HINGS OF STREET AND DESCRIPTION OF STREET AN
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional 3 -phosphoadenosine 5'-phosphosulfate synthethase 1 (PAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthethase 1) (PAPSS 1) (Sulfurylase kinase 1) (SK1) (SK 1) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate
                                                                                                                                                                                      5 KKOKTEN-----QOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLJGLSGAGKTTI°
                                                                                                                                                                                                VLPVSAEDKTRLEGCSKF:VLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM
                                                                                                                                                                                                                                                                                                                                                                                                            DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR
                                                                                                                                                                                                                                                                                                                                                                   TSF1SPFAKDRENARK1HESAGLPFFE1FVDAPLN1CESRDVKGLYKRARAGE1KGFTG1
                                                                                                                                                                                                                                                                                                                                                       239 AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
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         PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N->K: INCREASED ACTIVITY.
G->A: 30% DECREASE IN ACTIVITY.
H->A: LOSS OF ACTIVITY.
GH->AA: LOSS OF ACTIVITY.
L -> F (IN REF. 2).
MISSING (IN REF. 2 AND 3).
                                                                                                                                             624;
                                                                                                                                                                 Indels
                                                                                                                                             Length
                                                                                                               -> L (IN REF. 2).
6BC4F9648016CA31 CRC64;
                            PP-MOTIF (BY SIMILARITY).
H->A: LOSS OF ACTIVITY.
                                                                                                                                           79.4%; Score 2596; DB 1; 77.0%; Pred. No. 1.8e-179; ive 67; Mismatches 68;
 ATP (POTENTIAL)
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                    SIMILARITY).
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          FORMS
                                                                                                                                                                67;
                                                                                                                         70847 MW;
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624 AA;
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054820;
NP_BIND
ACT_SITE
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CONFLICT
SEQUENCE
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CONFLICT
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MUTAGEN
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phosphotransferase).
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Q92203:
 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 OKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSHAIP 72
                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: BELONGS TO THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF CYSTEINE AND METHIONINE, AND TO THE SULFATION OF PROTEINS, CARBOHYDRATES, LIPIDS, DRUGS AND XENOBIOTICS. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE APS KINASE
                                                                                                                                                                                                                                                SECOND STEP IS THE TRANSFER OF A PHOSPHATE GROUP FROM ATP TO APE Y IELDING 3. PHOSPHATE GROUP FROM ATP TO APE USED BY SULFOTRANSFERASE). IN MAMMALS, PAPE IS THE SOLE SOURCE OF SULFATE, APS APPEARS TO BE ONLY AN INTERMEDIATE IN THE SOLE SOURCE OF SULFATION PATHMAY. ALSO INVOLVED IN THE BIOSYNHESIS OF SULFATED. SELECTIN LIGANDS IN ENDOTHELIAL CELLS (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylysulfate.

CATALYTIC ACTIVITY: ATP + adenylysulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1997) to the EMEL/Genbank/VDBJ databases.
-!- FUNCTION: BIFUNCTIONAL ENYME WITH BOTH ATP SULEVELASE AND APS
KINASE ACTIVITY, WHICH MEDIATES TWO STEPS IN THE SULEATE
ACTIVATION PATHWAY. THE FIRST STEP IS THE TRANSFER OF A SULEATE
GROUP TO ATP TO YIELD ADENOSINE 5'-PHOSPHOSULFATE (APS), AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotidyltransferase; Kinase; Multifunctional enzyme;
              (APS kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORMS THE PHOSPHOSERINE INTERMEDIATE SIMILARITY).
                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                   Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia
 (SAT) (ATP-sulfurylase); Adenylylsulfate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.4%; Score 2563; DB 1; Length 624; 77.3%; Pred. No. 4.2e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADENYLYLSULFATE KINASE.
SULFATE ADENYLYLTRANSFERASE.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
             3'-phosphotransferase) (A'-phosphotransferase) (3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PP-MOTIF (BY SIMILARITY).
BF7461B4D07F2131 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                      phosphoadenosine-5'-phosphosulfate synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.2e
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002891; APS_kinase.
Interpro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002350; APS_kinase; 1.
ProDom; PD002381; ATP-sulfurylase;
             (EC 2.7.1.25) (Adenylylsulfate 3'-p. Adenosine-5'-phosphosulfate 3'-p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADENYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF004875; AAC02266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.
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                                                                                                                                                                    , Akita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIGRFAMS; TIGRO0455; apsK; 1
                                                                                                                                                                                                                                                                                                                                                                 phosphoadenylylsulfate.
                                                      OR PAPSS OR ATPSKÎ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                    STRAIN-NIH 2;
Venkatachalam K.V.
                                                                                                              NCBI_TaxID=10141;
transferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase;
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462;
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NP_BIND
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Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPERVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 VLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHALLMQDTCRRLLER 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTE 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 AAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAPKAWKVLTDYYRS 610
                                                              KTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAEAETLPSLSITKL
                                                                                                                                                                                                                                                                                                       DLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPIVLPVSAEDKTRLEG
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (All Sections)
50-MAY-2000 (All Sections)
51-MAY-2000 (All Sections)
52-MAY-2000 (Rel. 39, Created)
53-MAY-2000 (Rel. 39, Created)

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Eurotiales; Trichocomaceae; Emericella.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATI
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clarke D.L., Newbert R.W., Turner G.; "Cloning and characterisation of the APS kinase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 AA
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Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
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KAPS_PENCH
Q12657;
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  entities
                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                     Query Match
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                                                                                                                  ŝ
                                                                                                                                                                                                  135 IHE-----SAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETP 188
                                                                                                                                                              26
                                                                                                                                        STNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSHAIPCY
                                                                                                                                                      SLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENARK
                                                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duesterhoeft A., Philippsen P., "DNA sequencing and analysis of a 24.7 kb segment encompassing centromere CEN11 of Saccharomyces cerevisiae reveals nine previously
                                  ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoadenylylsulfate.
-!- PATHWAY: SECOND STEP IN THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korch C., Mountain H.A., Bystroem A.S.; "Cloning, nucleotide sequence, and regulation of MET14, the gene encoding the APS kinase of Saccharomyces cerevisiae."; Mol. Gen. Genet. 229:96-108(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                  11;
                                                                                            DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Adenyly1sulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                 16.2%; Score 529.5; DB 1; Lengun
51.4%; Pred. No. 2.9e.31;
Mismatches 57; Indels
           Cysteine biosynthesis; ATP-binding;
                                                           SIMILARITY).
6AADD483E2BCAICD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    Ą
                                                                                                                                                                                                                                                                                 ERVLKTNLSTVSDCVHQVVELLQEQNIV 216
                                                                                                                                                                                                                                                                                                       EVHVKNVDLPIQEAVKQIIDYLDSKKLL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91375456; PubMed=1654509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93070612; PubMed=1441752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown open reading frames.";
Yeast 8:749-759(1992).
                                                                      ..
ΜΕ
TIGRFAMS; TIGR00455; apsK; 1.
                                                                     23028
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                 38
             Transferase; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphotransferase).
                                                                     206 AA;
                                                                                                      Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                   31
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                       Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                  KAPS_YEAST
Q02196;
                                              ACT_SITE
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                                                                     SEQUENCE
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                                                                                           Query Match
                                  NP BIND
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   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GCTVWLTGLSGAGKTTISFALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 RIAEVAKLFADAGLVCITSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYKRARAGEIKGFTGIDSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penicillium chrysogenum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoadenylylsuifate.
--- PATHWAY: SECOND STEP IN THE SULFATE ASSIMILATION PATHWAY THAT LEADS TO THE BLOSYNTHESIS OF METHIONINE AND CYSTEINE.
--- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2010 (Rel. 39, Last annotation update)
50-Mosphosulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate xinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                             DiterPro; PR002931; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
Probom; PD002350; APS_kinase; 1.
TIGRFAMS; TIGR00455; apsk; 1.
Methionine biosynthesis; Cysteine biosynthesis; Transferase;
Kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
-1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
32F301FB6B2F41D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 1;
8.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 523;
                            or send an email to license@isb-sib.ch)
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requires a license agreement
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                                                                                  EMBL, X57990, CAA41055.1; --
EMBL, S55315; AAB19854.1; --
EMBL, X65124; CAA46252.1; --
EMBL, Z28001; CAA81833.1; --
PIR, S17244; S17244.
SGD; S0001484; MET14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 AA; 23060 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphotransferase).
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Foster B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5076;
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KAP2_ARATH
049196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                  STNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLV-SHAIPC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., A Zevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., A Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Giy B.J., Haga K., Halcch J., Harwood C.R., Henaut A., Julbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Aramanata D., Kasahara Y., Klaerr-Blanchard M., Kloetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Liu H., Mossell G., Mauel C., Medigue C., Median N., Mellado R.P., Milluo M., Mesti S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable adenylylsulfate Kinase (EC 2.7.1.25) (APS Kinase) (Adenosine-5'phosphosulfate Kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                               YSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENAR
                                                                                                                                                                                                                                                ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98015416; PubMed-9353932;
Roche B., Autret S., Levine A., Vannier F., Medina N., Seror S.J.;
A Bacillus subtilis chromosome segment at the 100 degrees to 102
degrees position encoding 11 membrane proteins.";
Microbiology 143:3309-3312(1997).
                                                                                                                                                       11;
                                                                                                                                                         Indels
                                      Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                     7DDC4BDA867FE7C2 CRC64;
                                                                                                                                DB 1;
                                                                                                                                                        29;
                                                                                                                             16.0%; Score 522.5; DB 1
50.0%; Pred. No. 9.5e-31;
                                                                                                                                                                                                                                                                                                                                                       PEVHVKNYELPVQDAVKQIIDYLDTKGYLP 207
                                                                                                                                                                                                                                                                                                                                                                                                                             199 AA
                                                                                                                                                                                                                                                                                                                                      PERVLKTNLSTVSDCVHQVVELLQEQNIVP 217
                                                                                                                                                        35; Mismatches
                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98044033; PubMed-9384377;
Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
TIGRFAMS; TIGR00455; apsK; 1.
                                                                                                       23770 MW;
                                                                                                                             Query Match
Best Local Similarity 50.09
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                39
                                                                                                       211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphotransferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                             107
                                                    Phosphorylation
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006735:
                                                                 NP_BIND
ACT_SITE
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                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENARKIH 136
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Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Stieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie T., Sanjan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Zumakoto H., Yamane K., Yashikawa H.F., Zumsteln E., Yoshikawa H.P., Zumsteln E., Yoshikawa H.P., Zumsteln E., Yoshikawa H.P., Zumsteln E., Yoshikawa H.D., Barchin A., The, Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Adenylyisulfate kinase 2, chloroplast precursor (EC 2.7.1.25) (APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probon; PD002350; APS_Kinase; 1.
TIGREAMS; TIGRO0455; ApsK; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90EC37FE4B02A123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOSYNTHETIC PATHWAY. SIMILARITY: BELONGS TO THE APS KINASE FAMILY
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47.0%; Pred. No. 3.7e-29;
tive 43; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 AA
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InterPro; IPR002891; APS_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997)
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REATING COLUMBIA S.

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RA PEDIT TO LOUGHER FROM N. A.

RA PROLITY DUSSIENCE THOSE TA A. SICHKEMEN W., DRILAN K.D., TERTYN N., HARTIS B., ANSORGE W., GEINCHELL L.A., Rieger M., HALTIS B., ANSORGE W., GEINCHELL L.A., RIEGER M., WOLLIER M., OLD SCHWIGHTEN J. SIMMERMEN TO S. SCHWIGHTEN J. SIMMERMEN W., MEDIGORNEOLD P. WALCON M., BOULTY M., BANCORGE Y., OCHUMBIA T., RESCHRICH E. PORTCELELE D. PETER-ALONSO M., BOULTY M., BANCORGE T., MEDIGORNEOLD P. WALCON M., SCHWIGHTEN P. T. STANDON J. STANDON J. AND SCHWIGHTEN T. A. MCCULLED D. T. SIMMERMEN M., MELLER S. Y. WOR STANDON J. AND SCHWIGHTEN T. A. MCCULLED D. T. STANDON J. A. STANDON J. A. WALCON E., RA MOSIGNED P. KIERD L.A. MCCULLED S. Y. A. MCCULLED S. Y. AND STANDON J. AND STANDON S. A. MCCULLED S. Y. AND STANDON J. AND STANDON S. A. MCCULLED S. Y. HEMPER S. Y. WAN STANDON S. Y. AND STANDON S. Y. MONITOR D. Y. HEMPER S. Y. HEMPER S. Y. WAN STANDON S. Y. MCOULLE S. Y. HEMPER S. Y. AND STANDON S. Y. MCOULT S. Y. HEMPER S. Y. HEMPER S. Y. AND STANDON S. Y. MCOULT S. Y. MONITOR M. M. ROGERS J. C. CICHER Y. Y. MONITOR M. N. AND STANDON S. Y. MCOULT S. Y. MONITOR M. M. MARTES A.C. SCHAMER M. Y. AND STANDON S. Y. RCCHMENT T. H. SCHAMEN W. PETERMEN S. AND STANDON S. Y. SCHAMEN S. Y. SCHAMEN S. Y. AND STANDON S. Y. SCHAMEN S. Y. SCHAM
                                                                                                                                                                                                                           Schiffmann S., Schwenn J.-D.;
"Isolation of cDNA clones encoding adenosine-5'-phosphosulfate-kinase (EC2.7.1.25) from Catharanthus roseus and an isoform (akn2) from
                                                  AANZ VA AIROSOFIU ON LOCATION.

ALABIDADSIS THALIANA (MOUSE-Ear Cress).

EUKATYOTA; VITIGIPLANTAE; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoadenylylsulfate.
PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Chloroplast (By similarity).
                   phosphosulfate 3'-phosphotransferase).
AKN2 OR AT4G39940 OR T5J17.110.
                                                                                                                                                                                                                                                                                                                In) Plant Gene Register PGR98-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNTHETIC PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:769-777(1999)
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                      eurosids II; Bra
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                            Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAKDRENARKIHESAGLP---FFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable adenylylsulfate kinase (BC 2, 7.1.25) (APS kinase) (Adenosine-
5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete grome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-431(2000).

-: FUNCTION: CATALYZES THE SYMTHESIS OF ACTIVATED SULFATE.

-: CATALYZIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masui N.,
                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Arami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                            71F1AD6E9B026886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPY 218
SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 PYEAPVNCEVVLKHTGDDESCSPRQMAE----NIISY
                                                                                                                                                                                                                                                                                                                                                                                      5e-29;
                                                                                                                                                                                                                                                                                                                                                                       Score 497.5; D. Pred. No. 9.5e-3; Mismatches
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                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                           EMBL; AF043351; AAC39520.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                            293 AA; 31977 MW;
                                                                                                                                                                                                                                                                                                                                                                        15.2%;
48.2%;
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                                                                                                                                                                                                                                                                                                               196
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                                                                                                                                                                                                                                                                                                  NP_BIND
ACT_SITE
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Matches
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MEDLINE-93075778; PubMed-1332767;
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                                                                                                                                                                                                                                                                                                                                                                                        HAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                     RENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETP 188
                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                            9 TENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                         Gaps
         PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                 Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p23846; Q59389; Q59376; P78105; 01-NOV-1991 (Rel. 20, Created) Clonvov-1991 (Rel. 20, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Adenyly1sulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'phosphosulfate sinase) (ATP adenosine-5'phosphosulfate sinase)
                                                                                                                                                                                            ProDom; PD002350; APS_kinase; 1.
TIGRFAMs; TIGR00455; apsK; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92268080; PubMed-1316900;
Leyh T.S., Vogt T.F., Suo Y.;
"The DNA sequence of the sulfate activation locus from
                                                                                                                                                                                                                                                                SIMILARITY).
6BB294F924F1FCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., CHARACTERIZATION, AND ACTIVE SITE
                                BIOSYNTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                               Score 487.5; DB 1;
Pred. No. 3e-28;
;; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200. AA.
                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                               14.9%; Score 487.5;
48.8%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 267:10405-10410(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                              Phosphorylation; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSC OR B2750 OR Z4058 OR ECS3604
                                                                                                                                                          EMBL; AP001512; BAB05208.1; -.
InterPro; IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
                                                                                                                                                                                                                                                                           202 AA; 22658 MW;
phosphoadenylylsulfate.
                                                                                                                                                                                                                                                                                                           Best Local Similarity 48.89
Matches 100; Conservative
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Satishchandran C., Hickman Y.N., Markham G.D.; "Characterization of the phosphorylated enzyme intermediate formed in the adenosine 5'-phosphosulfate kinase reaction."; Biochemistry 31:11684-11688(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coil ols7:H7 and genomic comparison with a laboratory strain K-12.":
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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-!- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-LE FLOW N.N. TEDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=111, Butland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Rochobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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InterPro; IPR002891; APS kinase.
Pfam; PF01583; APS_kinase; I.
ProDom; PD002350; APS_kinase; I.
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DNA Res. 8:11-22(2001).
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PIR; A44200; A44200
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KAPS_CATRO
049204;
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ACT_SITE
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                                                                                                                                                                                                                                                            136 HESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPERVLKTN 195
                                                                                                                                                                6 NVVWHSHPVTVQQR----ELHHGHRGVVLWFTGLSGSGKSTVAGALEEALHKLGVSTYLL 61
                                                                                                                                                   17 NVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSHAIPCYSL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brasslcales, Brasslcaceae, Arabidopsis.
                                                                                                                                                                                                              62 DGDNVRHGLCSDLGFSDADRKENIRRVGEVANLMVEAGLVVLTAFISPHRAERQMVRERV
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDINE-9434502; PubMed-8066145; Jain A., Leustek T.; adenylylphosphosulfate kinase from Arabidopsis "A CDNA clone for 5'-adenylylphosphosulfate kinase from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRATN=CV. Columbia;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylylsulfate kinase 1, chloroplast precursor (EC 2.7.1.25) (APS
kinase) (Adenosine-5 phosphosulfate kinase) (ATP adenosine-5'-
                                           41 ATP (BY SIMILARITY).

108 FORMS THE PHOSPHOSERINE INTERMEDIATE.

T -> Q (IN REF. 1).

22190 MW, 1106734E5935F414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leustek T.; Analysis of ATP-sulfurylase and APS-kinase genomic DNA sequences
                                                                                                                             6
                                                                                                    Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94325358; PubMed-8049272;
Arz H.E., Gisselmann G., Schiffmann S., Schwenn J.-D.;
"A cDNA for adenylyl sulphate (APS)-kinase from Arabidopsis
                                                                                                                             Indels
         Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                     DB 1;
                                                                                                                             26;
                                                                                                   14.6%; Score 476.5; DB 1 50.2%; Pred. No. 1.8e-27;
                                                                                                                                                                                                                                                                                                                                                                              276 AA.
                                                                                                                             35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphosulfate 3'-phosphotransferase).
AKN1 OR AT2G14750 OR F26C24.11 OR T6B13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1218:447-452(1994).
                   Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                            179 -QLVTNLVQQLLDLLRQNDII 198
                                                                                                                                                                                                                                                                                             196 LSTVSDCVHQVVELLQEQNIV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Physiol. 105:771-772(1994).
                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
TIGRFAMS; TIGRO0455; apsk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Landsberg erecta;
                                                                                                                           Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in Arabidopsis thaliana.
                                            41
108
133
            Kinase;
                                                                 133 1
200 AA;
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                             KAP1_ARATH
Q43295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana."
                                INIT_MET
NP_BIND
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                     Query Match
                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SGIKKOKTENOOKSTNVVYQAHHVSRNKRGOVVGTRGGFRGCTVWLTGLSGAGKTTISFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
              Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL). FORMS THE PHOSPHOSERINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                 phosphoadenylylsulfate.
-!- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Adenylylsulfate kinase, chloroplast precursor (EC 2.7.1.25) (APS
                                                                                                                                                                                              "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 476; DB 1; Length 276; 50.8%; Pred. No. 3.1e-27; ive 29; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                           -1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X75782; CAA53426.1; -.
EMBL; U05238; AAC50035.1; -.
EMBL; U59759; AAC50034.1; -.
EMBL; U59759; AAC24182.1; -.
Interpro; IPR002891; APS_Kinase.
Prodom; PF001583; APS_Kinase; 1.
TIGRRAMs; PIGG00455; apsK; 1.
TIGRRAMs; TIGR00455; apsK; 1.
TIGRRAMs; TIGR00455; apsK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSIT 1 37 ADENYLYLSULFATE KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB698643AA09D811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHETIC PATHWAY.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŗ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 50.8 95; Conservative
                                                                                                                                                                                                                                                                Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local 9
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    DDE DDE BERNAR REPRENTATION OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Schlffmann S., Schwenn J.-D.;
"Isolation of cDNA clones encoding adenosine-5'-phosphosulfate-Kinase (EC2.7.1.25) from Catharanthus roseus and an isoform (akn2) from Arabidopsis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIKKQKTENQQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPFAKDRENARKIHESAGLP - - FFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
FORMS THE PHOSPHOSERINE INTERMEDIATE (BY
                                                                 Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Usukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
  (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; Score 469.5; DB 1; Length 312; 47.7%; Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                        (In) Plant Gene Register PGR98-116.

-- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.

-- CATALYTIC ACTIVIT: AFP + adenylylsulfate = ADP + 3'-
phosphoadenylylsulfate.

-- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY.

REACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYS
BIOSYNTHEDIC PATHWAY.

-- SUBCELLULAR LOCATION: Chloroplast (By similarity).

-- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; Pubusass, ...
TIGRAMA; TIGROMAS; apsk; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
Phosphorylation; Transit peptide; Chloroplast.
TRANSIT 1 7 CHLOROPLAST (POTENTIAL).
312 ADENYLYLSULFATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16BBD11FB4B1FE27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDYEKPETPERVLKTNL --- STVSDCVHQVVELLQE 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                     phosphosulfate 3'-phosphotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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149
216
                                                                                                                                                               Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                     NCBI_TaxID=4058;
                                                                                                                                                               Vinceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDR 129
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=El Tor N16961, Serotype 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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NCBI_TaxID=666;
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PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. THIS PREACTION OCCURS EARLY IN THE REDUCTIVE BRANCH OF THE CYSTEINE BIOSYWTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'DNA sequence of both chromosomes of the cholera pathogen Vibrio
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylylaulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
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Pfam; PF01583; APS_kinase; 1.
Prodom: PD002350; APS_kinase; 1.
TIGRPAMs; TIGR00455; apsk; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
-!- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SUL-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP +
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л 1 6 09лк86	09JK86; 01-ост-2000 (тrEMBLrel.	01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation updat	Adenosine 5'-phosphosulfate kinase/ATP sulfurylase	Cavia porcellus (Guinea pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia NCBT mayIn=10141.	111	SEQUENCE FROM N.A.	da H., St	'Guinea piç	sulfurylase 2, gppAAPS synthase 2";	Submitted (	EMBL; AFZ31/98; AAF/0194.1;	InterFro; IPROUZBY1; APS_Kindse.	fam; PF015	Pfam; PF01747; ATP-sulfurylase; 1.	ProDom; PD002350; APS_kinase; 1.	ProDom; PD002381; ATP-sulfurylase;	TIGRFAMS; TIGRO0455; apsK; 1.	Kinase.	SEQUENCE	Query Match Best Local Similarity
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Kurima K., Singh B., Schwartz N.B.;
"Genomic organization of the mouse and human genes encoding the ATP Sulfurylase/Adenosine 5'-phosphosulfate kinase isoform SK2.";
D. Blol. Chem. 274:33306-3332(1999).
EMBL; AF172866; AAF12760.1; T.
EMBL; AF172867; AAF12760.1; JOINED.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
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Deyrup A., Schwartz N.B.;
"A member of a family of sulfate-activating enzymes causes murine
brachymorphism.",
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase/APS kinase isoform SK2 (EC 2.7.7.4)
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                                                                                                                                                                             DB 11; Length
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                                                                                                                                            Nucleotidyltransferase, Transferase.
; 621 AA; 70408 MW; 019519DC8E239F68 CRC64;
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Last annotation update)
                                                                                                                                                                           90.7%; Score 2965.5; DB 11
90.7%; Pred. No. 2.5e-230;
ive 21; Mismatchès 31;
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                  Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
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                                                                                                                                                                                              S., Tan Y.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.7%; Score 2638.5; DB 13; Lengt
79.3%; Pred. No. 5.6e-204;
.ive 60; Mismatches 66; Indels
                                                                                                                                                                                                                               human PTEN locus
PTEN function.";
                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002350; APS_Kinase; 1.
ProDom; PD002381; AFP=sulfurylase; 1.
TIGROMS; TIGROOMS; apsk: 1.
SEQUENCE 613 AA; 68948 MW; 28E50148377C4169 CRC64;
                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21455682; PubMed=11571655;
Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner
3'-phosphoadenosine 5'-phosphosulfate synthase 2.
                                                                                                                                                                                                                             "Conserved synteny between the Fugu and hun
evolutionary conservation of vertebrate PTI
oncogene 20:554-5561(2001).
EMBL; AF325922; AAL08416.1; -
InterPro; IPR002650; AFP-sulfurylase.
InterPro; IPR002650; AFP-sulfurylase.
PFam; PF01583; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
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                                                                                                                                                                                                                                                                                                          "Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPSS1) and PAPSS2: gene cloning, characterization and chromosomal localization."; Biochem. Biophys. Res. Commun. 268:437-444(2000).
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                                                                                                                             Homo sapiens (Human).
butaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                            Wood T.C.,
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                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-20145452; PubMed-10679223; Xu Z.-H., Otterness D.M., Freimuth R.R., Carlini E.J. Mitchell S., Moon E., Kim U.-J., Xu J.-P., Siciliano Weinshilboum R.M.;
                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
3' Phosphoadenosine 5'-phosphosulfate synthetase.
PAPSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodon; P10002350; APS_kinase; 1.
Prodon; P10002381; ATP-sulfurylase; 1.
TIGRFAMs; TIGR00455; apsK; 1.
SEGHENCE 624 AA; 70833 MW; A3DC9B943E68CDD6
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Pred. No. 5.1e-201;
 A.
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624
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InterPro; IPR002891; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PP01183; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     79.58;
77.18;
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                   096FB1;
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Strausberg R.;
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129 TSFISPYTQDRNNARQIHEGASLPFFEVFVDAPLHVCEQRDVKGLYKKARAGEIKGFTGI 188
                                     DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR 238
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                                                                                                                                                                                                                                                                           239 AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
                                                                                                                                                                                VLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM
                                                                                                                                                                                                                                                      359 VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAPQLRNPVHNGH
                                                                                                                                                                                                                                                                                                                            419 ALLMODICRRLLERGYKHPVLLLHPLGGWIKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV
                                                                                                                                                                                                                                                                                                                                                                                                  AIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase/APS Kinase.
ATP sulfurylase/APS Kinase.
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016496; AAD09325.1; -.
Interpro; IPR002891; APS_kinase.
Interpro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_kinase; 1.
ProDom; PF01747; ATP-sulfurylase; 1.
ProDom; PD002350; APS_kinase; 1.
ProDom; PD002350; APS_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 AA; 70881 MW; 0008DBC57B6F35BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.1%; Score 2588; DB 4;
76.6%; Pred. No. 6.8e-200;
Live 68; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deyrup A.T.;
"Human ATP sulfurylase/APS kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00455; apsK; 1
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|KAWTVLTEYYKS 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469; Conservative
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SEQUENCE
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                                                                                                                                                         ALLMQDICRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIV 478
                                                                                                                                                                                                                                                                                                                          TSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTG1 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPSS1) and .
PAPSS2: gene cloning, characterization and chromosomal localization.";
Biochem. Blophys. Res. Commun. 268:437-444(2000).
EMBL; AF105227; AAF40236.1;
Interpro; IPR002891; APS_kinase.
Interpro; IPR002505; APP-sulfurylase.
Pfam; PF01583; APS_kinase: 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                VLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM
                                                                                     VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH
                                                                                                                                                                                                                             479 AIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu Z.-H., Otterness D.M., Freimuth R.R., Carlini E.J., Wood T.C., Mitchell S., Moon E., Kim U.-J., Xu J.-P., Siciliano M.J., Weinshilboum R.M.;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002350; APS_Kināse; 1.
ProDom; PD002381; ATP-sulfurylase; 1.
TIGRPAMS; TIGR00455; apsk; 60DC9B943E7B75ED CRC64; SEQUENCE 624 AA; 70859 MW; 60DC9B943E7B75ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
37. phosphoadenosine 5'-phosphosulfate synthetase.
PAPSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 AA.
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609 KAWTVLTEYYKS 620
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Q9P1P9;
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Q9P1P9
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                      71 IPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRE 130
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                                                                                                                       KLDLOWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPIVLPVSAEDKTRL
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                                                                                                             VLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAEAETLPSLSIT
                                                                                                                                                                     EGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGDWLVGGD
                                                                                                                                                                                                                                              LOVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHALLMQDTCRRLL
                                                                                                                                                                                                                                                                                           ERGYKHPVLLLHPLGGWTKDDDVPLDWRWKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGP
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                                                                                                                                                                                                                                                                                                                                                                                   RVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAPKAWKVLTDYYRS
                                                                   NARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
Satoh N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of Brachyury downstream notochord genes in intestinalis embryo.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036852; BAB006291; -.
InterPro; IPR002891; APS. Rinase.
InterPro; IPR002860; ATP-sulfurylase.
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Last annotation update)
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ATP-sulfurylase;
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Pfam; PF01747; ATP-sulfurylase; 1.
ProDom; PD002350; APS_kinase; 1.
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ATP sulfurylase/APS kinase.
CI-ASAK.
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                                                                                                                                                                             368
SMALEEYLVCHGIPCYTLDGDNIRQGLNKNLGFSPEDREENVRIAEVAKLFADAGLVCI 128
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                     DSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVR
                                                                                                             AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPI
                                                                                                                                                       VLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKM
                                                                                                                                                                    VMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPS synthetase.
Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-NOV-1996 (TrEMBLrel. 01, Created). 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2367; DB 5;
Pred. No. 4.3e-182;
69; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenthal E., Leustek T.;
"A multifunctional Urechis caupo protein, PAPS
Pre sulfurylase and APS kinase activities.";
Gene 165:243-248(1995)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 AA
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PD002381; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002891; APS_kinase.
Interpro; IPR002650; ATP-sulfurylase.
Pfam; PP01583; APS_kinase; 1.
Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96096529; PubMed=8522184;
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Local Similarity (71.4%;)
hes 432; Conservabive 6
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                                                                                                                                                                                                                                                                                                                                                                                               KAWKVLTDYYRS 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6431;
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                                                                             70 AIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDR 129
                                                                                                                   ENARKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPE 189
                                                                                                                                                                                            TKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLDDGVINMSIPIVLPVSAEDKTR 309
                                                                                                                                                                                                                                                                               LERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYAG 489
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                                                     ENQOKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLTGLSGAGKTTISFALEEYLVSH
                                                                                                                                                                                                                                           RVLKTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIHELFVPENKLDHVRAEAETLPSLSI
                                                                                                                                                                    193 VVIKTADMPVEDCMMLVVKELMERNIIPCETTLPVMELFISHSQVGKKRAEAEALPSIDI
                                                                                                                                                                                                                                 LEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGDWLVGG
                                                                                                                                                                                                                                                                     DLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHALLMQDTCRRL
                                                                                                                                                                                                                                                                                                                                             PTEVQWHCRSRMIAGANFY IVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIP
                                                                                                                                                                                                                                                                                                                                                      FRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGENPPDGFMAPKAWKVLTDYYR
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chawez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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       618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LD25351p.
PAPS OR CG8363.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota; Metazoa; Arthropoda; Tracheata; Haschyoera; Musc
       Length
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
      5;
     Score 2233.5; DB 5;
Pred. No. 2.5e-171;
; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                       75;
      68.3%;
68.2%;
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                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
               Similarity
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                         410;
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      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLD--DGVI--N 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSIPIVLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKH 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHIKMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 KSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHP--ETKKD--LYEP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRMRKLAREGE 589
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(ATP-sulfurylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 VHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDP
                                                                                                                                                                                                                                                                                                                                 Gaps
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PAPS OR CG8363.

Drosophila melanogaster (Fruit fly).

Ekkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                Length 629;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                    6FF3F8797D98CCB3 CRC64;
                                                                                                                                                                                                                                                                             Query Match 62.3%; Score 2039; DB 5;
Best Local Similarity 63.1%; Pred. No. 1.2e-155;
Matches 392; Conservative 95; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630
EMBL; AY051724; AAK93148.1; -.
FlyBase; FBgn0020389; Paps.
InterPro; IPR002680; APS_kinase.
InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01583; APS_Kinase; 1.
ProDom; PD002250; APS_Kinase; 1.
ProDom; PD002250; APS_Kinase; 1.
ProDom; PD002380; APS_Kinase; 1.
TIGRPAMS; TIGR00455; apsk; 1.
SEQUENCE 629 AA; 71146 MW; 6FF97879;
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QVATNVTEQKHHVTRETRGKNLGLCRGFRGCTVWLTGLSGAGKTSIAFELEAYLVSRGIP

us-09-898-165b-7.rspt

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RESULT 11
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RA Adams W.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Adadon R.C., Rogers Y.-H.C., Blazej R.G., Champhe M., Fleiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Beeson K.Y. Benca P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Evakstein P., Botslakov S.,
Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Botchan M.R., Bouck J., Evakstein P., Brotlier P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Botlos B., Delcher A., Deng Z., Mays A.D., Davi I.S., Dietz S.M.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A dotak A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Ibeyama C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalazzolo M., Pittman G.S., Pan S., Pollard J., Purt V., Resen M.G.,
RA Shue B.C., Siden-Kiamos I. Singber M., Stupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
RA Shue B.C., Siden-Kiamos I., Singber M., Stups G., Zho Y., Zhu X., Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1-CATALYTIC ACTIVITY: ATP + SULFATE = DIPHOSPHATE + ADENYLYLSULFATE. EMBL; Y12861; CAA73368.1; -. EMBL; AE003515; AAF49102.1; ALT_SEQ. FlyBase; FBgn0020389; Paps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.1%; Score 2031.5; DB 5; Length 630; 63.4%; Pred. No. 5e-155; ive 94; Mismatches 116; Indels 13; Gaps
Diptera; Brachycera; Muscomorpha;
                                                                                                          Jullien D., Crozatier M., Kas E.; "cDNA sequence and expression pattern of the Drosophila melanogaster PAPS synthetase gene: a new salivary gland marker.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D688DC79DBBEDC76 CRC64;
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CONFLICT 270 270 MISSING (IN REF. 1).
                Ephydroidea, Drosophilidae, Drosophila.
NCBL_TaxID=7227;
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Interpro; IPR002650; ATP-sulfurylase.
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ProDom; PD002381; ATP-sulfurylase; 1.
  Endopterygota;
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Pfam; PF01747; ATP-sulfurylase; 1.
                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                          SEQUENCE FROM N.A. MEDLINE=98092112; Pubmed=9431815;
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Mech. Dev. 68:179-186(1997).
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  Pterygota; Neoptera;
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Best Local
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132
                                                         133 RKIHESAGLPFFEIFVDAPLNICESRDVKGLYKRARAGEIKGFTGIDSDYEKPETPERVL 192
                                                                                       197
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                            137
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198 NTHGYTVRESTQKLVTLEQEGIIPRS-LRDVDLLPELYPSESIATEALRHEAESLQAIE
               485 MLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHP--ETKKD--LYEPTHGGKVLSMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 CYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCITSFISPFAKDRENA
                                                                                                                       193 KTNLSTVSDCVHQVVELLQEQNIVPYTIIKDIH---ELFVPEN-KLDHVRAEAETLPSLS
                                                                                                                                                                                  249 ITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDTLLD--DGVI--NMSIPIVLPVSA
                                                                                                                                                                                                                                                                                                        WLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMNADAVFAFQLRNPVHNGHALLMQD
                                                                                                                                                                                                                                                                                                                                                                    425 TCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQHAAVLEEGVLDPKSTIVAIFPSP
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                                                                                                                                                                                                                                             305 EDKTRLEGCSKFVLAHGGRRVAILRDAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Interpro; IPR002891; APS_kinase.
Interpro; IPR002650; ATP-sulfurylase.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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Pfam; PF01747; ATP-sulfurylase; 1.
ProDom; PD002350; APS_kinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 WKVLTDYYRS 610
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SEQUENCE FROM N.A.
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al Similarity 63.4: 387; Conservative

Matches

us-09-898-165b-7.rspt

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478
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                                                                                                                                                                                    SDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPYTI -- IKDIHELFVPEN-KLDH 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHRKEERCSRVWGTTCTKHPHIKMYMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELK 394
                                                                                                                                                                                                                                                                                                                                                                                         395 QKCKEMNADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                  LDWRMKQHAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDP '514
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                                                                                      59
                                                                                                  14 MPMLKKPRYSSLSGQSTNITYQEHTISREERAAAVGRHEGFRGCTIWFTGLSGAGKTTIS 73
                                                                                                                              60 FALEEYLVSHAIPCYSLDGDNVRHGLNRNLGFSPGDREENIRRIAEVAKLFADAGLVCIT
                                                                                                                                                                                                                                314 GEKSDDKEDSWPMMDD-INQSIPIVLPISDDVKKGLEGVTRIALKYNGQVYALLSDPEIF
                                                                                     1 MSGIKKQKTEN-QQKSTNVVYQAHHVSRNKRGQVVGTRGGFRGCTVWLJGLSGAGKTTIS
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BEDLINE-28833795; Pubmed-9671738;
Kurima K., Warman M.L. Krishnan S., Domowicz M., Krueger R.C. Jr.
Deyrup A., Schwartz N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A member of a family of sulfate-activating enzymes causes murine brachymorphism.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                 28;
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                                             Length 652;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                 Indels
                       36148F20C31AD875 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
ATP sulfurylase/APS kinase isoform SK2 (EC 2.7.7.4)
                                          Query Match
57.7%; Score 1887; DB 5;
Best Local Similarity 56.5%; Pred. No. 2.3e-143;
Matches 362; Conservative 100; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:8681-8685(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AA
ProDom; PD002381; ATP-sulfurylase; 1.
TIGRFAMS; TIGR00455; apsK; 1.
SEQUENCE 652 AA; 72987 MW; 36148F.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase/APS kinase (AT3922890/F5N5_6) (Putative ATP
sulfurylase/APS kinase) (Putative ATP sulfurylase).
F5N5.6 OR AT3622890, F5N5.6 OR AT3622890.
Arabidopsis thaliam (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20026854; PubMed=10559207;
MEDLINE-20026854; PubMed=10559207;
MINIMA K., Singh B., Schwartz N.B.;
"Genomic organization of the mouse and human genes encoding the AID Sullarylase-Adenosine 5'-phosphosulfate kinase isoform SK2.";
"Genomic organization of the mouse and human genes encoding the AID Sullarylase, AEMP123801; JOINED.
EMBL; AF173361; AAF127801; JOINED.
EMBL; AF173362; AAF127801; JOINED.
EMBL; AF173362; AAF127801; JOINED.
INTERPO; IPR002650; AIP-sulfurylase.
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4,251,695 bp covered
                                                                                                                                                                                                                                                                                                                                                                                                  D75A2374E40C334F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1351.5; DB 4
pred. No. 8.7e-101;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                      Kinase; Nucleotidyltransferase; Transferase.
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"Structural analysis of Arabidopsis
Sequence features of the regions of
TAC and BAC clones.";
[3]
                                                                                                                                                                                                                                                                                                                          PD002381; ATP-sulfurylase;
                                                                                                                                                                                                                                                                                                   Pfam; PF01747; ATP-sulfurylase; 1.
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MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                  30142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.3%;
Best Local Similarity 95.5%;
Matches 254; Conservative
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Submitted (MAR-2000)
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Kaneko T., Kato 1
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NCBI_TaxID=3702;
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L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFVLAHG-GRRVAILRDAEFYEHRKEERC-342
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                                                                                                                                                                                                343 SRVWGTTCTKHPHI-KMVMESGDWLVGGDLQVLEKIRWNDGLDQYRLTPLELKQKCKEMN
                                                                                                                                                                               402 ADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMKQ
                                                                                                                                                                                                                                                           462 HAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPE
                                                                                                                                                                                                                                                                                                                                        522 TKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPAÄHNEFDFISGTRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIN=DESTREE: TISSUE=LEAF;
MEDLINE=95004649; PubMed=7920699;
Klonus D., Hoefgen K., Willmitzer L., Riesmeier J.W.;
Klonus D., Hoefgen K., Willmitzer L., Riesmeier J.W.;
"Isolation and characterization of two convaciones encoding ATP-
sulfurylase from Potato by complementation of a yeast mutant.";
Plant J. 6.105-112(1994).
EMBL; X75041; CAA52953.1;
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SEQUENCE 424 AA; 47519 MW; E82A27DC11350ABC CRC64;
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Last annotation update)
(EC 2.7.7:4).
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3e-96;
ches 81;
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61.7%; Pred. No. 3e-9
ive 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    582 RKLAREGENPPDGFMAPKAWKVLTDYYRS 610
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002650; ATP-sulfurylase. Pfam; PF01747; ATP-sulfurylase; 1. ProDom; PD002381; ATP-sulfurylase; 1. TIGRFAMS; TIGR00339; sopT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043170;
01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01, 01-JUN-2002 (TrEMBLrel. 21, 1) Sulfate adenylyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum (Potato).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                  286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Q43170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ELIVEEPKRREKKHEAADLPRVELTAIDLQWMHVLSEGWASPLGGFMRESEFLQTLHFNS 119
              Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,

Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,

Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Torlumi M.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

Hayashlzaki Y., Yu G., Yosesma E., Lam B., Lin J., Meyers M.C., Miranda M.,

Rawai J., Kim C., Kosesma E., Lam B., Lin J., Meyers M.C., Miranda M.,

Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,

Ecker J.R., Theologis A.,
                                                                                                                                                                                                                                SOUTDNICE FROM N.A.
SOUTDNICK A., Karlin-Neumann G.; Nguyen M., Idam B., Miranda M.,
Southnick A., Karlin-Neumann G.; Nguyen M., Idam B., Miranda M.,
Chau C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Kim C., Lin J., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Arabidopsis Open Reading Frame (ORF) Clones.",
Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai, Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satco M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Full Length cDNA of gene F5N5.6/AT3922890 (GI:11994718)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51459 MW; F05DFD8F86CF25C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 39.8%; Score 1301; DB 10; Il Similarity 62.7%; Pred. No. 2.4e-96; 244; Conservative 60; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002650; ATP-sulfurylase.
Pfam; PF01747; ATP-sulfurylase; 1.
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EMBL; AY091207; AAM14146.1; -
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                                                                                                                                                                             'Arabidopsis cDNA clones.
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Best Local (
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 NADAVFAFQLRNPVHNGHALLMQDTCRRLLERGYKHPVLLLHPLGGWTKDDDVPLDWRMK 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAAVLEEGVLDPKSTIVAIFPSPMLYAGPTEVQWHCRSRMIAGANFYIVGRDPAGMPHPE
                                                                                                                                                                                                                     TKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKAKKAMDFYDPARHNEFDFISGTRM
                                                                                                                                                                                                                                                         286 L-LDDG-VINMSIPIVLPVSAEDKTRLEGCSKFV--LAHGGRRVAILRDAEFYEHRKEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli are functionally equivalent but structurally and kinetically divergent: nucleotide sequence of two adenosine-5'-triphosphate-sulfurylase cDNAs from Arabidopsis thaliana and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 ELFVPENKLDHVRAEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMREKEYLQVMHFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last 'sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP sulfurylase precursor (EC 2.7.7.4).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GADAVFAFQLRNPVHNGHALLMTDTRRRLLEMGYKNPILLLHPLGGFTKADDVPLSWRMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a recombinant enzyme..;
Arch. Biochem. Biophys. 323:195-204(1995).
EMBL; UGG755, AAA92350.1;
InterPro; PR0020569; ATP-sulfurylase.
Pfam; PF01747; ATP-sulfurylase; 1.
Probom; PP002031 ATP-sulfurylase; 1.
TIGREAMS; TIGRE0039; SOPT; 1.
Chloroplast; Nucleotidyltransferase; Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96019964; PubMed=7487067;
Murillo M., Leustek T.;
"Adenosine-5'-triphosphate-sulfurylase from Arabidopsis thaliana "Adenosine-5'-triphosphate-sulfurylase from Arabidopsis thaliana and "Adenosine-5'-triphosphate-sulfurylase from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA
                                                                                                                                                                                                                                                                                                                                             RKLAREGENPPDGFMAPKAWKVLTDYYRS 610
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52029 MW;
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Best Local Similarity 62.3
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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465 AA;
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time Search Job time

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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US-09-898-165B-9 1845 Title: Perfect score:

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IDENTITY\_NUC Gapop 10.0 , Gapext 1:0 Scoring table:

2054640 segs, 14551402878 residues Total number of hits satisfying chosen parameters: Searched:

4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

GenEmbl:\*

gb\_ro:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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LOCUS
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM

Homo sapiens.

REFERENCE AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2014)
ul Haque, M. F., King, L. M., Krakow, D., Cantor, R. M., Rusiniak, M.E.,
Swank, R. T., Superti-Furga, A., Haque, S., Abbas, H., Ahmad, W.,
Ahmad, M. and Cohn, D. H.

QY         421 CTGCCATTCTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGCGTA 480           DD         111111111111111111111111111111111111	Oy 601 GACTGTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCCTATACTATA 660	781 AGGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTT 84	CGAGACGCTCGAATTCTATGAACACAGAAAAC 111111111111111111111111111111111		OY 1201 AATGCTGATGCGATGCATTGCATTGCGATGCCATGCCAT	1321 CTACACC 1401 CTACACC 1381 CAGCACG 1381 CAGCACG	OY 1441 TTTCCGTCTCCCATGTTATATGCTGGCCCCAAGAGGTCCAGTGGCACTGCAGGTCCCGG 150
TITLE Mutations in orthologous genes in human spondyloepimetaphyseal dysplasia and the brachymorphic mouse  JOURNAL NAT. Genet. 20 (2), 157-162 (1998)  MEDLINE 9842651  PUBBED 9771708  AUTHORS 1 to 2014)  AUTHORS 1 to 2014)  AUTHORS 1 to 2014)  TITLE Direct Submission JOURNAL Submission Location/Onalifiers Location/Onalifiers Location/Onalifiers	S .	VLTAINS LA LOIN-" MASCI KKOKTENOOKSTRIVVYOAHHVSRNKRGOVGTRGGERGCT VWLTGLSGAGKTTISFALEEYLUSHAIPCYSLDGDNYHGENBUGESPGDREENIRR IABVAKLFADAGLVOTTSFISSPAKDRENARKIHESAGLPFFEIFVDAPLNICESRDV KGLYKRARAGEIKGFTGIDSDYEKPETPERVLKTNLSTVSDCVHQVVELLQEQNIVPY IIKDIHELEVPPENKLDHVRAREAFILDSLSTRKIDLQWAVOYLESGWAPPLKGPRREKE YLQVMHFDYLLDDGVINMSTPIVLPVSAEDTREGCSKFVLAHGGRRVAILENDAEFY EHRKEERCSRVWGTTCTKHPHIKMVMSGGBJAUNGGDLQVLEKIRWNDGLDQYRLTPLE LKOKCKEMNADAVERFOLRHPYNHIKMVMSGGBJAUNGGDLQVLEKIRWNDGLDQYRLTPLE DDVPLDMRMKQHAAVLEGGVLDFKSTIVAIFPSPMLYAGETVGWHCKSRMIAGANFY IVGROPAGWPHPETKKDLYBETHGGRVLXSARPCILTSVEIIPRVAANNRAKKAMDFYD PARHNEFDFISGTRARKLAREGENPPDGFMAPKAWKVLTDYYRSLEKN"  ACTIALION ACTIA	BASE COUNT 515 a 492 c 33 g 474 t  ORIGIN  Query Match  Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	1 ATGTCGGGGATCAAGAAGCAGAAACCAGCAGAAATCCACCAATGTAGTCTAT 60 [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	121 CGAGGATGTACCGTGTGGCTAACAGGTCTCTGGTGCTGGAAAACAACGATAAGTTTT 180  [1111111111111111111111111111111111	241 GTCCGTCATGGCCTTAACAGAAATCTCGGATTCTCTCCTGGGACAGAGGAAAATATC 300	361 TITATITCTCCATICGCAAAGGATCGIGAGAAIGCCCGCAAAAIACATGAAICAGGGGGG 420 

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0.0 0.0 0.0 0.0 0.0 0.0 0.0	qa .	RESULT 2 BC009894 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNALL REMARK COMMENT	FEATURES	,

AF313907 Homo sapiens 3	mRNA, complete cds. v AF313907 AF313907.1 GI:12642583	Homo sapiens. M Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; E	Mammalia; Eutheria; Primates; Catarrhini; Homin 1 (bases 1 to 1845) Fuda, H., Shimizu, C. and Strott, C.A. Human Bifunctional 3'-Phosphoadenosine 5'-Phosp	Differential Expression of Activity Unpublished 2 (bases 1 to 1845)	Shimizu,C Direct Su Submitted		<ol> <li>1845 /function="catalyzes production of 3'-phosphoadenosine 5'-phosphosulfate, the universal sulfonate donor molecule, from inorganic sulfate and ATP"</li> </ol>	<pre>/codon_start=1 /prodouct="3'-phosphoadenosine 5'-phosphosulfate synthase 2 alpha" /protein_id="AAK00296.1"</pre>	/db_xref="G1:12642584" //translation="MSGIKKQYKTENQOKSTNVYYQAHHVSRNKRGQVVGTRGGFRGCT VMLTGLSGAGKTT1SFELBFYLVSHAIPCYSLDGDNVRHGLNRNLGFSFGDREENIRR IAEVAKLFADAGLVCITSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRDV	KGLYKRARAGEIKGFTGIDSDYEKPETPERVLKTNLSTVSCCVHQVVELLOEQNIVPY TIIKDIHELFVPENKLDHVRAEATLDSZITKLDLGWYQVLSEGWATPLKGFWREKE YLQVMHFDPILLDDGVVIMMSIPIVLPVSAEDKTRLEGCSKFVLAHGGRRVAILRDAEFY EHRKEERCSRVWGTTCTKHPHIKMVMGSGDWLVGGDLQVLEKIRWNDGLDQYRLTPLE		494 a tch	3; H	ATGTCGGGGATCANGANGCANGANGANGCANGANGANGANGANGANGANGANGANGANGANGANGANGA	61 CAGGCCCACCATGTGAGCAGGAATAAGAGAGGGCAAGTGGTTGGAACAAGGGGTGGGT	61 CAGGCCCACCATGTGAGCAGGAATAAGAGGGCCAAGTGGTTGGAACAAGAGGGGTGGGT		181 GCCTGGAGGAGATACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAAT 240	GTCCGTCATGGCCTTAACAGAAATCTCGGATTCTCTCCTGGGGACAGAGAGAAAATCTCTCCTGGGGACAGAGAGAAAATTCTCTCCTGGGGACAGAGAGAAAATTCTCTCCTGGGGACAGAGAGAAAATATCTTCTCTCTGGGACAGGGAAAATATCTCTCTGGGGAAAAATATCTCTCTGGGGAAAATATCTGGGAATGGCCTTAAAAAAAA	OTCOTORIGICALIRACAGAAALICICGGALICICCIGGGGACAGAGAGAAAALAITA
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Db   1381 CAGCACGCGCTGTGCTCGAGGAAGGGTCCTGGAT   1441 TTTCCGTCTCCCATGTTATATGCTGCCCCACAGAG   1441 TTTCCGTCTCCCATGTTATATGCTGCCCCACAGAG   1441 TTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAG   1501 ATGATTGCGGTGCCCATTTCTACATTGTGGGAGG   1501 ATGATTGCGGTGCCAATTTCTACATTGTGGGAGG   1501 ATGATTGCGGTGCCAATTTCTACATTGTGGGAGG   1501 GAAACCAAGAATGTTGTGGGAGG   1501 GAAACCAAGAAGGATCTGTATGACCCACTCATGGG   1501 GAAACCAAGAAGGATCTGTATGAACCCACTCATGGG   1501 GAAACCAAGAAGGATCTGTATGAACCCACTCATGGG   1501 GAAACCAAGAAGGATCTGTATGAACCCACTCATGGG   1501 GAAACCAAGAAGGATCTGTATGAACCCACTCATGGG   1611 HI	1621   GCCTCCACTTGTGAATCATTCCATTCCGAGTG   1681   GCCATGCACTTCTATGATCCATCCATTCCGATGAG   1681   GCCATGCACTTCTATGATCCAGCAGGCACAATGAG   1681   GCCATGCACTTCTATGATCCAGCAAGGCACAATGAG   1741   ATGAGGAAGCTTCCCCGGGAAGGAGGAATCCCCCA   1741   ATGAGGAAGCTCCCCGGGAAGGAAGCAATGATTATATACAGGTCCCCTGAGAGATTATTACAGGTCCCTGAGAGATTATTACAGGTCCCTGAGAGAGA	AF074331 Homo sapi AF074331 AF074331 Homo sapi Homo sapi Eukaryota Mammalia; I (bases Franzon, V and Suthe Direct Su Submitted Adelaide,	Source //crganism="homo sapiens" /db_xref="taxon:9606" /chromosome="10" /map="1043-24.1" 1. 37740423-24.1" 1. 37740423-24.1" /gene="PAPS2" /Godon_start=1 /product="PAPS synthetase-2" /product="PAPS synthetase-2" /product="A="A="A="A="A="A="A="A="A="A="A="A="A=
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S2) mRNA, complete <del>cds.</del>
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qa	0y 00 00	oy oy	Oy Oy	g oo oo	da da oy	yo.	Qy Qy Db	RESULT 5 AF173365 LOCUS DEFINITION ACCESSION VERSION VERSION	SOURCE SOURCE ORGANIS REFERENCE AUTHORE
E COUNT 1107 a 808 c 832;9 1027 t	Match   99.7%;   Score 1838.6;   DB 9;   Length 3774;		184 CGAGGAGGAGTACCTGTGGCTCTCTGGTGCTGGAAAACAACGATAAGTTTT 243  181 GCCCTGGAGGAGTACCTTGTCTCCCATGCCATCCTTGTTACTCCCTGGATGGGACAAT 240	304 GTCCGTCATGGCCTTAACACAAATCTCGGATTCTCTCGGGGACACAGAGGAAAATATC 363 301 CGCCGGATTGCTGAGGTGGCTAACGTGTTTGCTGTCTGGTCTGGTCTGGTTTACCAGC 360	TTTATTTCTCCATTGGCAAAGGATCGTGAGAATGCCCGCAAAATACATGAATCAGCGGGGCTGCCATTCTTTGAAATTTTGTAGATGCCCGCAAAATATTTGTAGAAGCAGGGCTGCATGCA	544 AAAGGCCTCTATAAAAAGGCCAGAGCTGGGGAGATTAAAGGATTTACAGGTATTGATTCT 603 541 GATTATGAGAAACTCCTGAGCGTGGCTTAAAACCAATTTGTCCACAGTGAGT 600 [		781 AGCGAAGGCTGGGCCACTCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTT 840 111111111111111111111111111111111111	901 CCCGTCTCTGCAGAGATAAGACACGGCTGGAAGGTGCAGCAAGTTGTCCTGGCACAT 960 [11]

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VWLTGLSGAGKTTISFALEBYLVSHAIPCYSLJGDNVRHGINRNLGFSPGDREBNIRR
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KGLYKRARAGEIKGFTGIDSDVEKPETPERVLKTNLSTYSDCYHQVVELLQEGNIVPY
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YLQVMHFDTLLDGMALPDGVINMSIPIVLPVSAEDKTRLEGCSKFVLAHGGRRVAILK
DAEFYEHRKEERCSRVWGTTCTKHPHIKMVMESGDWLVGGDLQVLEKIRWNDGLDQYR
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GWTKDDDVPLDWRMCQHAAVLEGGVLDPKSTLTVAIFBSPMLYAGPTBYQWHCRSRMIA
GANFY UYGRDPAGMHPETKKDLYEPPHGGRYLSMAGELTSVEIIPFRVAAYNKAKKA
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Location/Qualifiers
1. 1909
/organism="Homo sapiens"
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/dev stance="liver"
                                                                                        Kurima,K., Singh,B. and Schwartz,N.B.
Genomic organization of the mouse and human genes encoding
sulfurylaas/adenosine 5'-phosphosulfate kinase isoform SK2
J. Biol. Chem. 274 (47), 33306-33312 (1999)
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                causes
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                                     U.S.A. 95 (15), 8681-8685 (1998)
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/protein_id="AAF12761.1"
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"C_number="2.7.7.4"

/EC_number="2.7.1.25"

/note="bifunctional enzyme; alternatively
               enzymes
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Deyrup, A. and Schwartz, N.B.
A member of a family of sulfate-activating
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Direct Submission
Submitted (28-U)L-1999) Pediatrics, U
Maryland Ave. MC5058, Chicago, IL 606
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                                     Proc. Nati. Acad. Sci.
98337975
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YLQVMHFDTLLDGMALPDGVTNMSIPIVLPVSAEDTTREGGSKFVLAHGGRRVAILR
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/product="3'phosphoadenosine 5'-phosphosulfate synthase
                                                                                                                                                                                                                                                                                                                     Submitted (12-MAY-1999) Steroid Regulation, National Institute Health, 9000 Rockville Pike, Bethesda, MD 20892-4510, USA 3 (bases 1 to 2377)

Yenkatachalam, K.V., Fuda, H. and Strott, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-JAN-2001) Steroid Regulation, National Institute Health, 9000 Rockville Pike, Bethesda, MD 20892-4510, USA Sequence update by submitter of Sequence update by sequence version replaced g1:6642928.
                                                                               GGAATGCCCCATCCTGAAACCAAGAATCTGTATGAACCCACTCATGGGGGCAAGGTC
                                                                                                                                                    ATCTCAGGAACTCGAATGAGGAAGCTCGCCCGGGAAGGAGAATCCCCCAGATGGCTTC
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                          ACCATTGTTGCCATCTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGG
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Venkatachalam,K.V., Fuda,H. and Strott,C.A.
Direct Submission
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Catarrhini;
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/db_xref="GI:12484559"
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Mammalla, Eutheria, Primates,
1 (bases 1 to 2377)
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qq	861	AGCGAAGGCTGGGCCACTCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTT 920	LOCUS
Qy	841	ATGCACTTTGACACCCTGCTAGA	NOTESSED
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ογ	988	ATCCCOATTGTACTGCCCGTCTCTCCAGAGGATAAGACACGGCTGGAAGGGTGCAGGAAG 945	SOURCE ORGANISM
q <sub>Q</sub>	981	ATCCCCATTGTACTGCCCGTCTCTGCAGGATAAGACACGGCTGGAAGGGTGCAGCAAG 1040	
Qy	946	TTTGTCCTGGCACATGGTGGACGCAGGGTACCTATCTTACGAGACGCTGAATTCTATGAA 1005	REFERENCE
DÞ	1041	TTTGTCCTGGCACATGGTGGAGGGTAGCTATCTTACGAGACGCTGAATTCTATGAA 1100.	TITLE
Οy	1006	CACAGAAAAGGGGACGGTGTTTCGGGGGACAACATGTACAAAAACACCCCCAT 1065	JOURNAL
ορ	1101	CACAGAAAAGAGGAACGCTGTTCGCCGTGTTTGGGGGGACAACATGTACAAAACACCCCCAT 1160	AUTHORS
οy	1066	ATCAAAATGGTGATGGAAAGTGGCGCACTGCTGGTGGAGACCTTCAGGTGCTGGAG 1125	JOURNAL
qa	1161	ATCAAAATGGTGATGGAAAGTGGGGACTGGTTGGTTGGTGGAGACCTTCAGGTGCTGGAG 1220	REFERENCE
. δ	1126	AAAATAAGATGGAATGGATGGGCTGGACCAATACCGTCTGACACCTCTGGAGCTCAAACAG 1185	TITLE
QQ	1221	AAAATAAGATGGAATGATGGGTTGGACCAATACCGTCTGACACCTTTGGAGCTCAAACAG 1280	
δλ	1186	AAATGTAAAGAAATGAATGCTGATGCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCAC 1245	COMMENT
QQ	1281	AAATGTAAAGAAATGATGCTGTTTTTTTCATTCCAGTTGCGCAATCCTGTCCAC 1340	FEATURES
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Qy	1306	CACCGGGTCCTCCTACTACACCCTCTGGGCGGCTGGACCAAGATGACGATGTGCCTCTA 1365	
qq	1401	CACCCGGTCCTCCTACTACACCCTCTGGGCGGCTGGACGATGATGTGTGTTTTTT 1460	
Qy	.1366	GACTGGCGGATGAAGCAGCACGCGCTGTGCTCGAGGAGGGGTCCTGGATCCCAAGTCA 1425	
qq	1461	GACTGGCGGATGAAGCAGCACGCGCTGTGCTCGAGGAGGGGTCCTGGATCCCAAGTCA 1520	
. Оу	1426	ACCATGTTGCCATCTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGG 1485	
QQ	1521	ACCATTGTTGCTTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCACGTGG 1580	
Qy	1486	CACTGCAGGTCCCGGATGATTGCGGGTGCCAATTTCTACATTGTGGGGGGGG	
qa	1581	CACTGCAGGTCCCGGATGATTGCGGGTGCCAATTTCTACATTGTGGGGGGGG	
Qy	1546	GGAATGCCCCATCCTGAAACCAAGAACGTCTGTATGAACCCACTCATGGGGGCAAGGTC 1605	3'UTR
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qa	1761	AACAAAGCCAAAAAAAAGCCATGGACTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTC 1820	qq
οy	1726	ATCTCAGGAACTCGAATGAGGAAGCTCGCCGGGAAGGAGAGAATCCCCCAGATGGCTTC 1785	Qy
qa	1821	ATCTCAGGAACTCGAATGAGGAAGCTCGCCCGGGAAGGAGAATCCCCCAGATGGCTTC 1880	qq
Qy	1786	ATGCCCCCAAAGCATGGAAGGTCCTGACAGATTATTACAGGTCCCTGGAGAACTAA 1845	Qy
) <sub>B</sub>	1881	ATGCCCCCAAAGCATGGAAGGTCCTGACAGATTATTACAGGTCCCTGGAGAAGAACTAA 1940	qq
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DPEFYEHRVERCCRVWGTSSAKHPHVKMVMESGEMLVGGDLQVLERIRWNDGLDKYR LTPLEELKQKCKEMNADAVFARQLRNPVHNGHALLMQDTHRQLLERGYKHPVLLLHPLG GWTKDDDVPLDWRMKQHFAVLEGVLDFKSTIVAIFPSPMLYAGPTEVQMHCRCRMIA GANFYLVGRDPAGMPHETKRDLYEPTGRGVLSMAPGLTSVEIIFRVAATKVKKA MDFYNPERHDEFDFISGTRMRKLAREGENPPDGFMAPKAWKVLTDYYRSLEKIN" Fuda, H., Shimizu, C. and Stioll, .....

Direct Submission
Submitted (11-DEC-2001) Steroid Regulation, NICHD/NIH, Building 49,
Room 6A36, Bethesda, MD 20892-4510, USA
Sequence update by submitter
On Dec 11, 2001 this sequence version replaced gi:7804952.

Location/Qualifiers Submitted (04-APR-2000) Steroid Regulation, NICHD/NIH, Building 49, Room 6A36, Bethesda, MD 20892-4510, USA (bases 1 to 3480) /db\_xref="G1:7804953" /translation="MGCVKKQKTESQQKSTNVVYQAHHVSRNKRQQVVGTRGGFRGCT VM.TGLGGAGKTTISFALEEVLMSHAIPCYSLDGDNVRHGLMKNLGFSPGDREENIRR IAEVAKLFADAGLVCITSFISPFTKDRENARKIHESAGLPFFEIFIDAPLNICESRDV TIVKCIHELFVPENKLDQVRTEAESLPSLSITKLDLQWVQILSRGWATPLKGFMREKE YLQTLHFDTLLDGMVLRDGVINLSVPIVLPVSADDKARLEGCSEFALMYGGRRVAILC KGLYKRARAGEIKGFTGIDSDYEKPETPECVLKTNLTSVSDCVQQVVELLQEQNILPH 11-DEC-2001 68 ATGTCGGGGGTCAAGAAGCAGAAAGCCAACAGAAATCCACCACCAATGTGGTCTAC 127 121 CGAGGATGTACCGTGTGGCTAACAGGTCTCTGGTGGTGGAAAAACAACGATAAGTTTT 180 sulfurylase 181 GCCCTGGAGGAGTACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAAT 240 248 GCTCTGGAAGAGTACCTCATGTCCCATGCCATCCCATGCTACTCCCTGGATGGGGAAAT 307 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Hystricognathi; Cavlidae, Cavia. (bases 1 to 3480)

Fuda, H., Shimizu, C. and Strott, C.A.

Cloning and expression of guinea pig 3'-phosphoadenosine 5'-phosphosulfate (PAPS) synthase 2 9 1 ATGTCGGGGATCAAGAAGCAAAAGACGGAGAACCAGCAGAAATCCACCAATGTAGTCTAT Gaps /product="adenosine 5'-phosphosulfate kinase/ATP 15; ROD Length 3480; ארביבייה 3480 bp mRNA linear RO Cavia porcellus adenosine 5'-phosphosulfate kinase/ATF 2 mRNA, complete cds. Indels Score 1483; DB 10; Pred. No. 0; 0; Mismatches 210; 1. .3480 /organism="Cavia porcellus" /db\_xref="taxon:10141" /note="gpPAPS synthase 2" /codon\_start=1 922 sulfurylase 2" /protein\_id="AAF70194.1" 816 9 2 (bases 1 to 3480) Fuda, H. and Strott, C.A. Direct Submission AF251798.2 GI:17505184 Match 80.4%; ocal Similarity 87.9%; 1634; Conservative 1931. .3464 779 c .1930 .67 Cavia porcellus. 963 188 ce × Σ ĸ 2 5 g δ

> RESULT 7 AF251798

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QY         1306         CACCCGGTCCTCCTACTACACCCTCTGGGCGGCTGGACCAAGGATGACGATGTGCCTCTA         136           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1426 ACCATTGTTGCCATCTCCCATGTTATATGCTGGGGCCCCAGGGGCTCCAGTGCTCCAGTGCAGTCAGT	OY 1486 CACTGCAGGTCCCGGATGATTGCGGGTGCCAATTCTACATTGTGGGGACCCTGCA 1545	1628 GGAATGCCCCACCTGAGAACCAAGAACTGTATGAACCACCACCACCATGAAGGCAAGGTC 1606 TTGAGCATGGCCCTGGCCTCACCTCTGTGAAATCATTCCATTCGAGTGGTGCTACTACTACTACTACTACTACTACTACTACTACTACTAC	OY 1666 ACCAARCCAARGACTTCTATGAARCCAGGGCAARGACTTCTTTTTTTTTT	Oy 1786 AIGGCCCCCAAAGCATGGAAGGTCCTGACAGATTATTACAGGTCCCTGGAGAACTA 1844	RESULT 8 AF085144 AF085144 2000 bp mRNA linear ROD 30-DEC-1998	AF085144.  AF085144.1 GI:4038345		REFERENCE 1 (bases 1 to 2000) AUTHORS ul Haque,M.F., King,L.M., Krakow,D., Cantor,R.M., Rusiniak,M.E., Swank,R.T., Superti-Furga,A., Haque,S., Abbas,H., Ahmad,W., Ahmad,M. and Cohn,D.H.	TITLE Mutations in orthologous genes in human spondyloepimetaphyseal dysplasia and the brachymorphic mouse JOURNAL MAT. Genet. 20 (2), 157-162 (1998)	PUBMED 9771708  PUBMED 9771708  REFERENCE 2 (bases 1 to 2000)  AUTHORS ul Haque, M.F., Kingy, L.M., Krakow, D., Cantor, R.M., Rusiniak, M.E., Swank P. T. Ginorti-Enrola A. Hanne C. Abhas H. Ahmad W.	Ahmad, M. and Cohn, D.H.  TITLE Direct Submission JOURNAL Submitted (20-AGC-1998) Pediatrics (Medical Genetics), Cedars-Sinai Medical Center, 8700 Meverly Blvd, Los Angeles, CA 90048, USA		/db_xref="taxon:10090" /chromosome="19" /map="32 cM" /tissue_type="spleen"
GTCCGTCAT           GTCCGTCAC	301 CGCCGGATTGCTGAGGTGGCTAAGCTGTTTGCTGGTCTGGTCTGCATTACCAGC 360  11111111111111111111111111111111111	1 CTGCCATTCTTGAAATATTTGTAGATCCACCTCTAAATATTTGTGAAGCAGAGACGTA	481 AAGGCCTUTATAAAGGCCAGAGGTTAAAGGATTAAAGGATTTACAGGTATTATACAGTATTT 540	601 GACTGTGCCCCAGGTAGGAACTTCTGCAAGAGCAGAACATTGTACCCTATACTATA 660 [1111111   1   1   1   1   1   1   1   1	1 GCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTTTG	781 AGGGAAGGGTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTT 840 	41 ATGCACTTTGACACCCTGCTAGATGATGGCGTGATCAACATGAGC	ATCCCCATTGTACTGCCGTCTCTGCAGAGATAAGACACGGCTGGAAGGGTGCAGGAGGTGCAGGAGGGTGCAGGAGGGTGCAGGAGGGTGCAGGGGGGGG	TITGLCEGGAATGGIGGACGGAGGTAGCTATCTTACGAGACGCTGATTCTATGAATTCTATGAATTCTATGAATTCTATGAATTCTATGAATTCTATGAATTCTACGAGGACGCGAGGAGGAGGATTTTATGTGACCCTGAATTCTACGAG	1006 CACAGAAAAGGGAACGCTGTTCCCGTGTTTGGGGGACAACATGTACAAAACACCCCCAT 1065 	1066 ATCAAAATGGTGATGGAAAGTGGGGACTGGCTGGTGGAGCCTTCAGGTGCTGGAG 1125 	AAAA   11 AGAA	1186 AAATGTAAAGAAATGGTGATGCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCAC 1245    1  1  1  1  1  1  1  1  1  1  1  1  1	1246 AATGGCCATGCCCTGTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGGCTACAAG 1305 

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                                                         /product="ATP sulfurylase/APS kinase 2"
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TTIRGTHELEYPENKVDGIRAEAFTLESLPTKTDLGWQUISGGWAPPEK
EYTGYLHFDTLLDDGYTNAEAFTLESLPTKTDLGWQUISGGWAPPEK
EYTGYLHFDTLLDDGYTNAETPILVLPVSSDDSKALEGCSKFALMYEGREVALLODPER
YEHRKEERCSRVWGTATAKHPHIKMVMESGDMLVGGDLQVLERIRWDDGLDQYRLTPL
EXTGXCKNAMNDAVFRACLRNPVHOGHALLMQDTRRALLEGYKHPVLLLHPLGGWTK
DDDVPLEMRNKQHAAYLERFVLDFKSTIVAFFRRALEGYKHPVLLAGANF
YLVGRDPAGMPHPETKKDLYEFFYLDFKSTIVAFFSPMLYAGFTEVGWTK
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Pred. No. 0;
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       /gene="Atpsk2"
/note="Asapk2"
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  CGTGTGCCTAACAGGTCTCTCTGGTGCTGGAAAAACAACGATAAGTTTTGCCCTGGAGGA
                                                                                                                                                                                      GTACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCATGG
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RIAEVARLFADAGLVCITSFISPFAKDRENARKIHESAGLPFFEIFVDAPLNICESRD
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HTTIKGIHELEVPERKVDQIRAEAFTLPSLPTTKIDLGWVQILSEGRATPLKGFWREK
EYLQTLHFDTLLDGVVPRDGYINMSIPIVLPVSADDKARLEGCSKFALMYEGRRVALL
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RLTPLELKQKCKDMNADAVFAFQLRNPVHNGHALLMQDTRRRLLERGYKHPVLLLHPL
                                                                                          ROD 27-JUL-1998
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AGANFYIVGRDPAGMPHPETKKDLYEPTHGGKVLSMAPGLTSVEIIPFRVAAYNKIKK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/EC_number="2.7.7.4"

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/EC_number="2.7.4"

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/EC_number="2.7.4"

/EC_number="2.7.4"

/EC
1 (bases 1 to 1996)

Kurima,K., Warman,M.L., Krishnan,S., Domowicz,M., Krueger,R.C.
Deyrup,A. and Schwartz,N.B.
A member of a family of sulfate-activating enzymes causes murir
                                                               TCGCCCGGGAAGGAGAATCCCCCAGATGGCTTCATGGCCCCCAAAGCATGGAAGGTCC
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Submitted (04-MAR-1998) Kennedy Center, U. of Chicago, 5841
Maryland Ave. MC5058, Chicago, IL 60637, USA
Location/Qualifiers
1. 1996
/organism="Mus musculus"
/organism="Mus musculus"
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Kurima, K.
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JOURNAL Submitted (25-AUG-1995) James R. Mensch, Pediatrics, University of Chicago, 5841 S. Maryland Ave. MC5058, Chicago, IL 60637, USA Location/Qualifiers  Location/Qualifiers 1. 2479 /organism="Mus musculus"	CDS 34. 1908  Anote="blinnctional enzyme; mediates two steps in sulfate activation: transfer of a sulfate group to ATP by ATP sulfurylase (ATP sulfate adenylyltransferase, EC 2.7.7.4)	to yield adenosine 5'-phosphosulfate (APS), and the subsequent transfer of a phosphate group from ATP to APS by APS kinase (ATP adenosine-5' phosphosulfate 3'-phosphotransferase EC 2 7 1 25) vielding ADP and	3'-phosphosdenosine-5'-phosphosulfate (PAPS)" /codon_start=1 /product="ATP sulfurylase/APS kinase"	/processor.ref="672:1109676" /db xref="672:1109676" /translation="MEIPGSLCKKVKLSNNAQNWGMQRATNVTYQAHHVSRNKRGQVV /translation="MEIPGSLCKKYKLSNNAQNWGMQRATNVTYQAHHVSRNKRGQVV GTRGGFRGGTWWLYGLSGACKTTVSWALEEYLVCHGTPCYTLDGDNIRQGRNKNLGFS	PEDIREN VRA PRACHADACUCLIST IST TYDRINGNYOLHEGASDIE FEVV DA PELINCEO, NORVINGNYOLO VOLO VOLO VOLO VOLO VOLO VOLO VOLO	VALLENPEFFERENCAROWGITCKNHPY IKWU-EGGDWLLGGLLCOLLOFIERTEWORG LDOOYELTPTELKOKENCHMADAVFAFOLRNPVHGHALLWOTHKOLLERGYRRPVLL LHPLGGWTKDDVPLMWRMKOHAAVLEEGILDDETTVVAIFPSPMMYAGPTEVOWHCR ARWYAGANFY TYGRDPAGMPHPETGKDLFYPFHGATUTMAGPTEVOWHCR VYZYNANYVEGHURDANDAYFAKANNYVENTANANNYVENTANANNYVENTANNY	polyA_site	Match 54.5%; Sco	Best Local Similarity 71.7%; Pred. No. 4.5e-276; Matches 1317; Conservative 0; Mismatches 520; Indels 0; Gaps 0; ·  Qy 9 GATCAAGAAAAGACGGAGAACCAGCAGAAATCCACCAATGTAGTCTATCAGGCCCA 68		132 CCATGTCAGCAGGAATAAGAGGGCAGGTGGTGGGGGAACCAGAGGTGGCTTCCGTGGTTG 19	192 CACAGTTTGGCTGAGTTTGTCCGGAGCAAGACGACGTGAGCATGGCTTGGA	QY 189 GGAGTACCTTGTCTCCCATGCCATCCCTTGTTACTCCTGGATGGGGACAATGTCCGTCA 248	Qy 249 TGGCCTTAACAGAAATCTCGGATTCTCCTGGGGACAGAGAAATATCCGCGGGAT 308	Oy 309 TGCTGAGGTGGCTAAGCTGTTTGCTGATGCTGGTCTGGATTACCAGCTTTATTC 368	OY 369 TCCATTCGCAAAGGATCGTGAGAATGCCGCGAAAATACATGAATCAGCAGGGCTGCCATT 428	OY 429 CTTTGAAATATTGTAGATGCACCTCTAAATATTGTGAAAGGACGAAAAGGCCT 488	Qy 489 CTATAAAAGGGCCAGAGCTGGGGAGATTAAAGGATTTACAGGTATTGATTCTGATTATGA 548
Db 1225 GATGGAAAGTGGGGACTGGTTGTTGGTGGACCTACAGGTGCTAGAGAATAAGGTG 1284  Qy 1137 GAATGATGGGCTGGACCAATACCGTCTGACACCTCTGGAGCTCAAACAGAAATGTAAAGA 1196  L	1197	Qy 1257 CCTGTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGCTACAAGCACCCGGTCCT 1316	QY 1317 CCTACTACACCCTCTGGGCGCTGGACCAAGATGACGATGTGCCTCTAGACTGCGGGGT 1376	OY 1377 GAAGCAGCAGCAGCTGTCCTCGAGGACGGGTCCTGGATCCCAAGTCATTGTTGC 1436	Oy 1437 CATCTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTC 1496	OY 1497 CCGGATGATTGCGGGTGCCAATTTCTACATTGTGGGGAGGGA	QY 1557 TCCTGAAACCAAGAACTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGGC 1616	QY 1617 CCCTGGCCTCACCTCTGGAAATCATTCCATTCCGAGTGGCTGCCTACAACAAAGCCAA 1676  1	Qy 1677 AAAAGCCATGGACTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTCATCTCAGGAAC 1736	OY 1737 TCGAATGAGGAAGCTCGCCGGGAAGGAAGAATCCCCCAGATGGCTTCATGGCCCCCAA 1796  11	AGCATGGAAGTTCTGACAGATTATTACAGGTCCCTGGAGAAGAACTA 1844		RESULT 10 MM034883 LOCUS MM034883 DEFINITION MUS MUSCUlus ATP sulfurylase/APS kinase mRNA, complete cds. ACCESSION U34883			and Schwartz, N.B. The isolation and characterization of cDNA encoding the mouse bifunctional ATP sulfurylase-adenosine 5'-phosphosulfate kinase	JOURNAL 0. BLOI. CHell. 2/U (49), 29433-29439 (1993) MEDLINE 96094345 PUBMED 7493984 REFERENCE 2 (bases 1 to 2479)	Men

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Db 1865 GCTGACAGAATACTACAAATCCTTGGAGAA 1894	RESULT 13	Z	625	NISM Unknown. NISM Unclassified. NCE 1 (bases 1 to 2506)	Debuilder, N.C. hilliman, J.L., Hawails, F.K., Guegler, K.J. and Corley, N.C. bisease related nucleotide kinases Patent: US 5817482-A 4 06-007-1998; Patent: US 5817482-A 4 06-007-1998;	rce 1.2506 /organism="unknown" NT 704 a 500 c 592 g 710 t	Query Match Query Local Similarity 71.3%; Score 990; DB 6; Length 2506; Best Local Similarity 71.3%; Pred. No. 8.9e-272; Matches 1305; Conservative 0; Mismatches 255; Indels 0; Gaps 0;	9 GATCAAGAAGCAAAAGACGGAGAACCAGCAGAAATCCACCAATGTAGTCTATCAGGCCA 68	69 CCATGTGAGGAATAAGAGGGGCAAGTGGTTGGAACAAGGGGTGGGT	129 TACCGTGTGGCTAACAGGTCTCTGTGGTGCTGGAAAAACAACATTTTGCCCTGGA	189 GGAGTACCTTGTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCGTCA 	249 TGGCCTTAACAGAAATCTCGGGATCGGGGACAGAGGAAAATATCGCCGGAT 		369 TCCATTCCCAACGATCGTGAGAANGCCCGCAAAATCATGAATTCACGAGGTTTCCTTT.  434 ACTTACACTCACGAACAATGCAAGGCAAAATCATGAAGTGAAGTTTACCTCTAACATTCATCAAGAAGCAAAATCATCATGAAGTGAAGTTTACCGTTT		CTATAAAAGGGCCAGAGCTGGGGAGATTAAAGGATTTACAGGTATTGATTATGATTATGA 	549 GAAACCIGAAACTCCIGAGCGIGGCTIAAAACCAAITIGICCACAGIGAGIGACIGIGI	609 CCACCAGGTAGTAGCATTCTGCAGAACATGTACCTATACTATAATCAAAGA	DD 6/4 CCAGCAAGIIGIGGAACIICIACAGGAACGGGAIATIGIACCIGIGGAIGCAICITAIGA 733

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	72 93 99 99 84	1000 TIGGGCAACCCATTGAATGGCTTATGAGAGAGGGAGTACTTGCAGTGCCTTCATTT 1059  849 TGACACCCTGCTAGATGATGGCGTGATCAACATGGAGTACTTGCAGTGCCTTCATTT 1059  1060 TGATTGTCTTCTGGATGAGGGTGCATTAACTTGTCAGTACTTATGGATGCGAC 1119  909 TGCAGAGGATAAGACGGTGGAGGGTGCAGAGTTTGTCCTGATGGTGCAGG 968  1100 TGCAGAGGATAAGACAGGTTGAAGGTTGTCTGACTGTGACGGGGGGGG		6 0	1089 GGACTGGCTGGTGGAGACCTTCAGGTGCTGGAGAAATAAGATGGATG	1149 GGACCAATACCGTCTGACACCTCTGGAGCTCAAACAGAAATGTAAAGAAATGCTGA 1208 	1209 IGCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCA 1268 	1269 GGACACCTGCCGCAGGCTCCTAGAGGGGCTACAAGCACCCGGTCCTCCTACTACTACCC 1328	1329 TCTGGGCGGCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGATGAAGCAGCACGC 1388 	1389 GGCTGTGCTCGAAGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCATTTTCCGTC 1448 	1449 TCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCAGTGCAGGAGGTCCGGATGC 1508	1509 GGGTGCCAATTCTACATTGTGGGGAGCGCTCCTGCAGGAATGCCCCATCCTGAAACCAA 1568 	1569 GAAGGATCTGTATGAACCCACTCATGGGGCAAGGTCTTGAGCATGGCCCCTGGCCTCAC 1628 	1629 CTCTGTGGAAATCATTCCGAGTGGCTGCCTACAACAAGCCAAAAAAGCCATGGA 1688 
qo oy	6 9 6 8	9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	oy g	Qy dg	Oy Dp		QQ D	Qy Dp	У да	Qy Dp	do Db	QY	Qy	Qy
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Db 1814 ACTTGCTCGAGAAGGCCAGAAACCACCTGAAGGTTTCATGGCTCCCAAGGCTTGGACGT 16  Qy 1809 CCTGACAGATTATTACAGGTCCCTGGAGAA 1838	RESULT 14  AX281701 LOCUS DEFINITION Sequence 110 from Patent W00177389. ACCESSION AX281701. G1:16608952 KEYWORDS SOURCE HOMO Sapiens CONGANISM HOM SAPIENS CONGANISM HOMO SAPIENS CONG	ο · ε. ο · ·	/organism="Homo sapiens" /db_xref="taxon:9606" /note="Incyte ID No: 238824.2" BASE COUNT 715 a 566 c 634 g 727 t 4 others ORIGIN	Query Match 53.7%; Score 990; DB 6; Length 2646; Best Local Similarity 71.3%; Pred. No. 8.9e-272; Matches 1305; Conservative 0; Mismatches 525; Indels 0; Gaps	4 68     27	12 33	18 39.	24	QY 249 TGGCCTTAACAGAAATCTCGGATTCTCTCTGGGGACAGAGAAATATCCGCGGAT 308	Qy         309 IGCTGAGGTGGCTAAGCTGTTTGCTGATGCTGGTCTGGTC	42	GCCT 48	ATGA 54	GTGT 60

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BYTCKNHYYTKMWEGOMILGGDLGVLDRYVNDGLDGYTRTPTERKOFKKONNAD
AVFAROLRNYYTKMYMEGOMILGGDLGVLDRYVRNDGLDGYTRTPTERKDDDVPLAWRRKQ
HAAVLEEGVLNPETTVVAIFPSPMWYAGPTEVOWHCRARMVAGANFYIVGRDPAGMPH
PETGKOLYEEGHGARVLTAMAPCLITLEIVPFRYAAYNKKKRMDYYDSEHHEDFEFIS
GTRARKLARGGVRPEGFMAPKAMYLTEYYKSLEKA"
175 C 70 TO
      PENKLHLAKTDAETLPALKINKVDMQWVQVLAEGWATPLNGFMREREYLQCLHFDCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 ATGCTACACTCTGGATGGTGACAATATTCGTCAAGGTCTCAATAAAAATCTTGGCTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TAAAACCAATTTGTCCACAGTGAGTGACTGTGTCCACCAGGTAGTGGAACTTCTGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 GAAAACAGACTCCTGTGATGTAAATGACTGTGTCCAGCAAGTTGTGGAACTTCTACAGGA
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ed. No. 2.2e-271;
Mismatches 509;
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Best Local Similarity 71.8%;
Matches 1294; Conservative
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TYSWALLESTLYCHGTHVSTYLDGDNTRANGGSPEDREBNYRRIAEVARATE
GLVGITSSTSPYTORNNARQIHEGASLPFFEVFVDAPHVCEORDVKGLXKKARAGE
IKGFTGIDSEYEKPEAPELVLKTDSCDVNDCVQQVVELLQERDIVPVDASYEVKELYV
                                                                                                                                                                                                                                                                                                                                                                   BC011392 2430 bp mRNA linear PRI 30-JUL-2001
Homo sapiens, Similar to PAPS synthetase, clone MGC:9898
IMAGE:3869484, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be found
CACTITIGGAAATAGTICCCTTTCGAGTIGCAGCTTACAACAAGAAAAAAAGAAGCGTATGGA 1899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-ULL-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: i.Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   `.
3
                                             CTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTCATCTCAGGAACTCGAATGAGGAA
                                                                                    GCTCGCCCGGGAAGGAGAATCCCCCAGATGGCTTCATGGCCCCCCAAAGCATGGAAGGT
                                                                                                                                                        Lu, X., G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Similar to PAPS synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="MGC:9898 IMAGE:3869484"
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/db_xref="G1:15030252"
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/db_xref="taxon:9606"
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KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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GTGCAGCAAGTTTGTCCTGGCACATGGTGGAGGGGGGGGG	ACACCCC 	GGTGCTGGAGAAAAAAGATGGAATGATGGCTGGACCAATACCGTCTGACACCTCTGGA	GCTCAAACAGAAATGTAAAGAAATGAATGCTGATGCGGTGTTTGCATTCCAGTTGGCGAA 	TCCTGTCCACAATGGCCATGCCGGTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAG	GGGCTACAAGCACCGGTCCTCCTACTACACCCTCTGGGCGGCTGGACCAAGGATGACGA [	TGTGCCTCTAGACTGGCGGATGAAGCAGCACGCGGCTGTGCTCGAGGAGGGGTCCTGGA 	TCCCAAGTCAACCATTGTTGCCATCTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGA	GGTCCAGTGGCACTGCAGGTCCCGGATGATTGCGGGGTGCCAATTTCTACATTGTGGGGAG	GGACCCTGCAGGAATGCCCCATCCTGAAACCAAGAAGGATCTGTATGAACCCACTCATGG	GGGCAAGGTCTTGAGCATGGCCCCTGGCCTCTGTGGAAATCATTCCATTCCGAGT 	GGCTGCCTACAACAAAGCCAAAAAGCCATGGACTTCTATGATCCAGCAAGGCACAATGA 	GTTTGACTTCATCAGGAACTCGAATGAGGAAGCTCGCCGGGAAGGAGAGAATCCCCC	AGATGGCTTCATGGCCCCCAAAGCATGGAAGGTCCTGACAGATTATTACAGGTCCCTGGA 	GAA 1838 	
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Search completed: June 4, 2003, 16:43:26 Job time: 4822 secs Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

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Transferase; TRNSFS-6; human; antitumour; cancer; inflammation; gastrointestinal disorder; developmental disorder; genetic disorder; neurological disorder; reproductive disorder; smooth muscle disorder; immunological disorder; gene therapy; diagnosis; ATP sulfurylase/APS kinase 2; ss.
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                                                                                                                                                                                                 The present sequence is that of cDNA clone 1420940CB1 encoding human transferase TRNSFS-6 (see AAY79214), 1 of 15 claimed human transferase proteins of the invention (see AAY79209-23). The clone was isolated from foetal kidney cDNA library KIDNNOT09. TRNSFS-6 is expressed in cardiovascular, gastrointestinal, reproductive and endocrine tissues, especially those associated with cancer, inflammation and cell proliferation. It shows homology to ATP sulfurylase/APS kinase 2. A polynucleotide comprising nucleotides 942-986 of the present sequence can be used as a DNA probe. The
                                                                                                                                                                                                                                                                                                                                 new human transferase proteins and the polynucleotides encoding them can be used in the diagnosis, prevention and treatment (including gene therapy and antisense therapy) of cancer, developmental disorders, gastrointestinal disorders, genetic disorders, immunological disorders, neurological disorders, reproductive disorders, and smooth muscle disorders.
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Matches 1841;
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	429 CTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGAGTGTAAAAGGCCT 488	GAAACCTGAAACTCTGAGGGTGTGCTTAAAACCAATTTGTCCACAGTGAGTG	669 TATCCACGACTCTTGTGCCGGAAAACAAACTTGACCACGTCCGAGCTGAAGCTGAAAC 728 	729 TCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTTTGAGCGAAGG 788	849 TGACACCTGCTAGATGGCGTGATCAACATGAGCATCCCCATTGTACTGCCCGTCTC 908	999 CCGTTTGTCTTCTTCTTCTTGTTTTTTTTTTTTTTT	### ### ##############################
9	oy ob	90 OV	QV Db	OY OY OY	oy oy oy	0	6 q
Db 1713 TTGAGCATGGCCTCACCTCGTGGAAATCATTCCATTCCGAGTGGCTGCTAC 1772  Qy 1666 AACAAAGCCAAAAAACGACTTCTATGATCCAGCAAGGCACAATGACTTTGACTTC 1725	RESULT 2 AAX84897  ID AAX84897 standard; cDNA to mRNA; 1875 BP.  XX AC AAX84897; XX  DT 24-SEP-1999 (first entry)	Human APS kin APS kinase/AT 3'-phosphoade Homo sapiens.	PN JP11187883-A XX PD 13-JUL-1999. XX PF 26-DEC-1997; 97JP-0360387.	26-DEC-1997; (NIRA ) UNITIKA (HUMA-) ZH HUMA WPI; 1999-45154	XX  New human-derived APS kinase/ATP sulfurylase gene - useful for PT large scale preparation of 3'-phosphoadenosine 5'-phosphosulfate PT (PAPS)  XX  Claim 3; Page 7-8; 9pp; Japanese.  XX  CT his sequence encodes the human-derived APS kinase/ATP sulphurylase of CC This sequence or codes the human-derived APS kinase/ATP sulphurylase of CC 5'-phosphosulphate (PAPS) on a large scale prepare 3'-phosphoadenosine CC 5'-phosphosulphate (PAPS) on a large scale	Sequence 1875 BP; 526 A; 379 C; 499 G; 471 T; 0 other; Sequence 1875 BP; 526 A; 379 C; 499 G; 471 T; 0 other;  Duery Match Bast Local Similarity 71.3%; Pred. No. 5.4e-295; Matches 1305; Conservative 0; Mismatches 525; Indels 0; Gaps	QY         9 GATCAAGAAGACGAGAACCAGCAGAATCCACCAATGTAGTCTATCAGGCCCA 68           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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P-PSDB; AAW70494.
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                                                                          TCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCGGATGATTGC 1508
                                                                                                         1509 GGGTGCCAATTTCTACATTGTGGGGAGGGACCCTGCAGGAATGCCCCATCCTGAAACCAA 1568
                                                                                                                                               Human disease related nucleotide kinase-2; DRNK-2; deoxyguanosine kinase;
p21ras; cell proliferation; oncogenesis; cancer; gene therapy;
immune disorder; neurological dysfunction; ss.
                                                     GCCTGTGCTCGAGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCATCTTTCCGTC
               TCTGGGCGCCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGGATGAAGCAGCACGC
                                                                                                                  GAAGGATCTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGGCCCCTGGCCTCAC
                                                                                                                                                                     CTTCTATGATCCAGCAAAGGCACAATGAGTTTGACTTCATCTCAGGAACTCGAATGAGGAA
                                                                                                                                                                                                                                 1749 GCTCGCCCGGGAAGGAGAATCCCCCAGATGGCTTCATGGCCCCCAAAGCATGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                 Human disease related nucleotide kinase-2 (DRNK-2) DNA sequence
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                                                                                                                                                                                                                                                                        GCTGACAGAATACTACAAATCCTTGGAGAA 1868
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The present sequence represents a human disease related nucleotide
Kinase-2 (DRNK-2) DNA sequence first identified in Incyte Clone
X13887 from the lung tissue colNA library (LUNGNOT 02). The DNKR-2 DNA
sequence is useful for the production of the corresponding recombinant
cenzyme. The invention provides DRNK enzymes, which are deoxyguanosine
Kinases, which catalyse the transfer of a terminal phosphate from
adenosine triphosphate (ATP) or guanine riphosphate (GTP) to guanosine
or guanidine in the regulation of cellular levels of GTP and its
corresponding nucleoside triphosphate. As GTP levels are known to
corresponding nucleoside triphosphate. As GTP levels are known to
corresponding nucleoside triphosphate. As GTP levels are known to
corresponding nucleoside triphosphate. As GTP levels are known to
corresponding nucleoside triphosphate. As GTP levels are known to
control the activity of certain oncogenic proteins oncogenesis.
Corresponding seases (e.g. cancers, immune disorders and neurological
dysfunction) related to this lack of activity may be prevented or
treated with the recombinant enzyme, or by gene therapy based strategies.
Anti-sense constructs of the DNKR encoding nucleic acids may also be
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                                 caused
Nucleic acids encoding de:oxy:guanosine kinase - useful for recombinant production of the enzyme for treating diseases callack of the enzyme e.g. cancers caused through loss of enzyme
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Pred. No. 6.4e-295;
0; Mismatches 525;
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ilarity 71.3%;
Conservative
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Matches 1305; Conserv
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX00602) for increasing the stability of the fused The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAX0611-X00724; amino acid sequences AAX0611-X00724; amino acid sequences AAX061807-w68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in
  immune diseases, inflammation or blood disorders
                                                           English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (see AAX00611 for described uses).
                                                     265-267; 385pp;
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Sequence 2527 BP; 706 A; 508 C; 597 G; 716 T; 0 other;

ö 128 248 308 188 333 393 368 453 428 488 573 633 809 693 899 813 GATCAAGAAGCAAAAGACGGAGAACCAGCAGAAATCCCACCAATGTAGTCTATCAGGCCCCA TACCGTGTGGCTAACAGGTCTCTCTGGTGCTGCAAAAACAACGATAAGTTTTGCCCTGGA GGAGTACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCA TGGCCTTAACAGAAATCTCGGATTCTCTCCTGGGGACAGAGGAAAATATCCGCCGGAT AGGTCTCAATAAAAATCTTGGCTTTAGTCCTGAAGACAGAGAAGAAGAATGTTCGACGCAT CGCAGAAGTTGCTAAACTGTTTGCAGATGCTGGCTTAGTGTGCACATCACAAGTTTCATATC CTATAAAAGGGCCAGAGCTGGGGAGATTAAAAGGATTTACAGGTATTGATTCTGATTATGA CCAGCAAGTTGTGGAACTTCTACAGGAACGGGATATTGTACCTGTGGATGCATCTTATGA TCCATTCGCAAAGGATCGTGAGAATGCCCGCAAAATACATGAATCAGCAGGGCTGCCATT CTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGACGTAAAAGGCCT AAAGCCAGAGGCCCCTGAGTTGGTGCTGAAAACAGACTCCTGTGATGTAAATGACTGTGT CCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCCTATAATCAAAGA TATCCACGAACTCTTTGTGCCGGAAAACAAACTTGACCACGTCCGAGCTGAGGCTGAAAC AGTAAAAGAACTATATGTGCCAGAAAATAAACTTCATTTGGCAAAAACAGATGCGGAAAC Gaps ; Length 2527; Indels Score 990; DB 20; Pred. No. 6.4e-295; ); Mismatches 525; ; 53.7%; 71.3%; Conservative Best Local Similarity Matches 1305; Conserv σ 129 249 334 69 189 274 394 454 429 574 549 514 489 694 754 Query 염 g ŏ g g Dp ò à 셤 ò ò οy ò g ò g Qγ g οy g ò g ά

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generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAX08011-X00724; amino acid sequences AAX08004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypectides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                   94 GAGCAATAACGCGCAGAACTGGGGAATGCAGAGGCAACCAATGTCACCTACCAAGCCCA 153
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                                                                                                                                                                                                                          Score 990; DB 20;
Pred. No. 6.4e-295;
); Mismatches 525;
                                                                                                                                                                     (see AAX00611 for described uses).
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71.3%;
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                                                                                                                                                                                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsectorlast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The gene number, and the clone it is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The gene can be used to
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Ni J, Olsen HS;
    1809 CCTGACAGATTATTACAGGTCCCTGGAGAA 1838
                                                                                                                                                                                                 Human secreted protein gene 76 clone HOSFD58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebner R, Ferrie AM,
Lafleur DW, Moore PA,
, Shi Y, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted human protein. The gene number, a
from, are detailed in the descriptor line.
                     Claim 1; Page 234-236; 385pp; English
                                                                                                        AAX00686 standard; DNA; 2527
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                               CCGTGTGGCCATTCTTCGCAATCCACAGGTTTTTTGAGCACAGGAAAGAAGGAGCGCTGTGC
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249 TGGCCTTAACAGAAATCTCGGATTCTCTCCTGGGGACAGAGGAGAAATATCCGCCGGAT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful for diagnosis of conditions, disorders or diseases associated with atheroscierosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atheroscierosis, cerebral stroke, and cardiovascular disorders such as PCR primers and probes. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are als bolynucleotide sequences of the invention which are differentially expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 AGGTCTCAATAAAAATCTTGGCTTTAGTCCTGAAGACAGAGAAGAGAAATGTTCGACGCAT
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                                                                                                                                                                                                                                                                                                                                                                                       Mikita
                                                                                                                                Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                Human DNA sequence #110 expressed during foam cell differentiation
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Pred. No. 6.6e-295;
0; Mismatches 525;
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detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                ACTIGCTCGAGAAGGCCAGAAACCACCTGAAGGTTTCATGGCTCCCAAGGCTTGGACGT
                                                 GGGTGCCAATTTCTACATTGTGGGGGGGGGCCCTGCAGGAATGCCCCATCCTGAAACCAA
                                                                                        GAAGGATCTGTATGAACCCACTCATGGGGGCCAAGGTCTTGAGCATGGCCCCTGGCCTCAC
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GGCTGTGCTCGAGGAAGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCATCTTTCCGTC
           TCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCGGATGATTGC
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genes from Drosophila and
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                                            The sequence data for this patent did not form part of the prințed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                             532 T; 0 other;
                                                                                                                Score 634; DB 23;
Pred. No. 7.8e-185;
0; Mismatches 695;
                                                                                          2463 BP; 579 A; 667 C; 685 G;
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Best Local Similarity 60.7%;
Matches 1124; Conservative 0
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                                                                                                                                                                                                                                                                                                and cell-cell
                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signalling and cell
                                     developmental biology; cell signalling; insecticide;
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            123 AGCGGGAAAGACTACTGTGAGCATGGCCTTGGAGGAGTACCTGGTTTGTCATGCTATCC
                                                      216 TTGTTACTCCCTGGATGGGGACAATGTCCGTCATGGCCTTAACAGAAATCTCGGATTCTC
                                                                                                                                                                         TCCTGGGGACACAGAGGAAAATATCCGCCGGATTGCTGAGGTGGCTAAGCTGTTTGCTGA
                                                                                                   TGCTGGTCTGGTCTGCATTACCAGCTTTATTTCTCCATTCGCAAAGGATCGTGAGAATGC
                                                                                                                                                                                                                      156 TGCTGGAAAAACAACGATAAGTTTTGCCCTGGAGGAGTACCTTGTCTCCCATGCCATCCC
                                                                                                                                            GCAGAACATTGTACCCTATACTATAATCAAAGATATCCACGAACTCTTTGTGCCGGAAAA
                                                                                                                                                                                                                                                                                                                                                                   663 TAAACTTTGGCAAAAACAGATGGGGAAACATTACCAGCAGTGAAAATTAATAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAGGATTTACAGGTATTGATTCTGATTATGAGAAACCTGAAACTCCTGAGCGTGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 7588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCTATGAACACAGAAAAGAGGAACGC 1023
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                                                                                                                                                      1435 ATCTCGGGAACCAAGATGCGCACCCTGGCCAAAACGGGAGCCAGTCCGCCGGATGGCTTC
                                                                  1555 TAGCCGAATGTAAAATGGATATTTTTTTTTTAGATCCTGCCCTTCCGTGTTGCTGCCCTAT
                                                                                                         1615 AGATGGCCCAGGGACTAGACATGGAGGTAAGGGTACCACTGCCTAATCGGCCAAATC
                                                                                              AACAAAGCCAAAAAAGCCATGGACTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTC
                                                                                                                                         ATCTCAGGAACTCGAATGAGGAAGCTCGCCCGGGAAGGAGAATCCCCCCAGATGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment of human adenosine 5' phospho:sulphate kinase - used a probe in the detection of genetic disease and for the production of 5' phospho:sulphate kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307;
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        GCATGGCCCCTGGCCTCACC-
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metabolic pathway; promoter; termination sequence; ss.
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990S-0127462.
990S-0128234.
990S-0128714.
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99US-01349
                         Arabidopsis thaliana
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1263
1027 TCCCGTGTTTGGGGGACAACATGTACAAAACACCCCCATAT---CAAAATGGTGATGGAA 1083
                                                                                                                                                                                ATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGGCTACAAGCACCCGGTCCTCCTACTA 1323
                                                                                                                                                                                                                            CACCCTCTGGGCGGCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGATGAAGCAG 1383
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             .084 AGTGGGGACTGGCTGGTTGGTGGAGACCTTCAGGTGCTGGAGAAATAAGATGGAATGAT
                                                        1212 GAGAAGAGAACTATATGATCCTGATCATGGAAAGAGAGTCTTAAGCATGGCCCCTGGA
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Pred. No. 1.3e-107;
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59.6%;
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Best Local Similarity 59.6'
Matches 705; Conservative
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1739 GAATGAGGAAGCTCGCCCGGGAAGGAGAGAATCCCCCAGATGGCTTCATGGCCCCCAAAG 1798
1910 CCAATGCTGGAAATTGGTTGATTGGGGGTGACCTAGAGGTCATTGAACCAATTCAGTACA 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer cell line Km12L4-A cDNA library derived sequence #978.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2270 TATTCCCATCTCCCATGCACTATGCTGGACCCACGGAGGTGCAGTGGCATGCCAAAGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mapping;
                                     2030 GCAATGCGGGATGCTGTGTTTGCCTTCCAGCTCCGGAATCCTGTTCACAATGGCCATGCTT
                                                                                                                                                                                                             1319 TACTACACCCTCTGGGCGGCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGATGA
                                                                                                                                                                                                                                                                                                                                                                TCTTTCCGTCTCCCATGTTATATGCTGGCCCCCACAGAGGTCCAGTGGCACTGCAGGTCCC
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                                                                                                                 TGAATGCTGATGCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCC
                                                                                                                                                                                         TGTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGGGCTACAAGCACCCGGTCCTCC
                                                                                                                                                                                                                                                                                          AGCAGCACGCGCTGTGCTCGAGGAAGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAACCAAGAAGGATCTGTATGAACCCACTCATGGGGGCCAAGGTCTTGAGCATGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cancer; malignant; chromosome cell line Kml2L4-A; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1799 CATGGAAGGTCCTGACAGATTATTA 1823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH31044 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200018916-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963 -TGGACGGAGGGTAGCTATCTTACGAGACGCTGAATTCTATGAACACAGAAAAGAGGAAC 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 TGGAAAGTGGGGACTGGCTGGTTGGTGGAGACCTTCAGGTGCTGGAGAAATAAGATGGA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                (SAMS) promoter fused to two soybean conditions are including and a second encoding cystathionine-gamma-synthase (CGSI) were inserted into binary vectors for Arabidopsis transformation. The SAMS promoter is active in seedlings and callus and over-expression of a gene in embryo stage can be achieved at an early developing stage using the SAMS promoter may be used as an alternative to cauliflower mosaic virus 35s promoter may be used as an alternative to cauliflower mosaic virus 35s promoter to drive expression of selectable marker genes. Plant cells transformed with the SAMS constitutive promoter are useful for increasing or decreasing the expression of heterologous nucleic acid fragments in a plant, preferably corn, rice, wheat, barley, safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous nucleic acid fragments include herbicide resistance or pathogen resistance nucleic acid fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904
                                                                                                                                                                                                                                                                                                                                                                                                    Expression cassettes comprising the S-adenosyl-L-methionine synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTCTGCAGAGGATAAGACACGGCTGGAAGGGTGCAGCAAGTTTGTCCTGGCACATGG--
                                                                                                                                                                                                                                                                                S-adenosyl-L-methionine synthetase promoter for expressing target heterologous herbicide-resistance or pathogen-resistance nucleic acid fragments in plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1490 TCGTGGAGCTTGTGGTGACGGATTTTGAGAGGGATTTGAAGAAGGAGGGTGAGGCTCTTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTTTGAGCGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1550 TGCCGAGGATCAAGCTCTCAAGGATTGACCTTGAGTGGGTCCATGTCCTCAGCGAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTTATGCACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 ACACCCTGCTA----GATGATGCCGTGATCAACATGAGCATCCCCATTGTACTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3684;
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Pred. No. 4.1e-107;
0; Mismatches 455;
                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 48-49; 50pp; English.
                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.8%;
Best Local Similarity 59.9%;
Matches 698; Conservative (
                                                                                                                               98US-0113045
                                                                                           99WO-US30180
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               WO200037662-A2
                                                                                           17-DEC-1999;
                                                                                                                               21-DEC-1998;
                                                     29-JUN-2000
                                                                                                                                                                                                         Falco SC,
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AAH31145 standard; cDNA; 401

RESULT 13

AAH31145

AAH31145;

Labat I;

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useful cancer

Sudduth-Klinger J;

Kassam

16

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The present invention describes a library of polynucleotides comprising 1079 nucleotide sequences (given in AAH30067 to AAH3145). Also described are: (1) an isolated polynucleotide (1) having at least 90% identity to one of the 1079 sequences; (2) a recombinant host cell containing (1); cone of the 1079 sequences; (2) a recombinant host cell containing (1); (3) an isolated polypeptide (11) encoded by (1); (4) an antibody that specifically binds to (11); (5) a vector comprising (1); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by 65 of the 1079 sequences given in the specification. The polynucleotides are used to monitor patients having (or susceptible) to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. The polynucleotides are also useful for monitoring the efficacy of various therapies and preventive interventions. Polynucleotide probes based on the disclosed sequences are useful for chromosome mapping and detection of transcription levels. The 1079 polynucleotide sequences were derived from a human colon cancer can
                                                                                                                                                                                                                                                           J, Innis MA, Garcia PD, Sudduth-Kling
Randazzo F, Kennedy GC, Pot D, Kassam
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide library comprising 1079 defined sequences, the form of an array to detect cancer or susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 463; 502pp; English
98US-0102180.
98US-0102380.
98US-0103815.
98US-0105877.
                                                                                                                                                                                                                                                              Escobedo
                                                                                                                                                                                                                                                                                                                                                       Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                     Giese K,
Drmanac R,
                                                                                                                                                           CHIR ) CHIRON CORP.
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                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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28-SEP-1998;
29-SEP-1998;
08-OCT-1998;
27-OCT-1998;
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Reinhard C,
Lamson G, D
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Sequence 401 BP; 82 A; 116 C; 118 G; 85 T; 0 other;

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1329
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                                               1210 GCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCAG 1269
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                                                                                            1270 GACACCTGCCGCAGGCTCCTAGAGAGGGGCTACAAGCACCCGGTCCTCCTACTACACCCT
                                                                                                                                                                                                                                                        GACACTCGCCGCAGGCTCCTAGAGAGGGGCTACAAGCACCCGGTCCTCCTACTACACCCT
                                                                                                                                             CTGGGCGCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGATGAAGCAGCACGCG
                                                                                                                                                          GCTGTGCTCGAGGAAGGGGTCCTGGATCCCAAGTCAACCATGTTGCCATCTTTCGGTCT
                                                                                                                                                                                                                   GCTGTGCTCGAGGGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCATCTTTCCGTCT
                                                                                                                                                                                                                                           1450 CCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCGGATGATTGCG
                          Gaps
                          1;
 DB 21; Length 401;
                          Indels
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Pred. No. 2.2e-106,
0; Mismatches 7;
20.5%;
ilarity 98.0%;
Conservative 0
            Similarity
                       394;
Query Match.
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1210 GCGGTGTTTGCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCAG 1269

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Indels

Length 401;

21;

Score 378.8; DB 21; Pred. No. 2.2e-106; ); Mismatches 7;

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Conservative

Local Similarity

Match

Matches 394;

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360

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20.5%; 98.0%;

(Revised entry submitted to correct SQ line format.) Sequence 401 BP; 82 A; 116 C; 118 G; 85 T; 0 other; 9

1270 GACACCTGCCGCGGGGCTCCTAGAGGGGGGTACAAGCACCCGGTCCTCCTACTACACCCT 1329

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The present invention describes a library of polynucleotides comprising are: (1) an isolated polynucleotide (1) having at least 90% identity to one of the 1079 sequences; (2) a recombinant host cell containing (1); (3) an isolated polypeptide (II) encoded by (I); (4) an antibody that specifically binds to (II); (5) a vector comprising (I); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by 65 of the 1079 sequences given in the specification. The polynucleotides are used to monitor patients having (or susceptible) to cancer to detect containing a part used to monitor patients having (or susceptible) to cancer to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interventions. Polynucleotide probes based on the disclosed sequences are useful for chromosome mapping and detection of transcription levels. The 1079 polynucleotide sequences were derived from a human colon cancer cell line Km12L4-A cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potentially malignant events at a molecular level before they are detectable at a gross morphological level. The polynucleotides are also useful for monitoring the efficacy of various therapies and preventive
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                                                                                                                                                         Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping;
detection; colon cancer cell line Km12L4-A; ss.
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                                                                                                                     colon cancer cell line Km12L4-A cDNA library derived seg#1079.
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Randazzo F, Kennedy GC, Pot D., Kassam
Crkvenjakov R, Dickson M, Drmanac S, L
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide library comprising 1079 defined sequences, the form of an array to detect cancer or susceptibility to
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98US-0102180.
98US-0102380.
98US-0103815.
98US-0105877.
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                                                                    (updated)
(first entry)
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON COR! (HYSE-) HYSEQ INC.
                                                                                                                                                       Human; diagnosis;
                                                                                                                                                                                                                                           WO200018916-A2.
                                                                                                                                                                                                            Homo sapiens.
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08-OCT-1998;
27-OCT-1998;
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27-JUL-2001
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Database

Result No.

ENERAL UNFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.

APPLICANT: Hawkins, Phillip R.

APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

APPLICANT: GOFIEV, Neil C.

TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12

ADDRESSEE: Incyte Pharmaceuticals, Inc. COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
CLASSIFICATION NUMBER: US/08/879,561
FILING DATE: HEREWITH
APPLICATION NUMBER: 34749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749 STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 SEQUENCE CHARACTERISTICS: LENGTH: 2506 base pairs TYPE: nucleic acid STRANDEDNESS: single INFORMATION FOR SEQ ID NO: ; LIBRARY: LUNGNOT02 ; CLONE: 373887 US-08-879-561-4 IMMEDIATE SOURCE:

Appl Appli Appli

US-09-103-840A-2 US-09-103-840A-1 US-09-040-738-1 US-08-652-426A-1 US-08-206-176-1

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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 89, Appli

Sequence 1 Sequence 1 Sequence 1 Sequence J

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Patent No. 633866
GENERAL INFORMATION:
APPLICANT: Allan, Steve
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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Pred. No. 5.5e-107;
0; Mismatches 473;
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APPLICANT: Falco, Carl
TITLE OF INVENTION: Genes Encoding Sulfate,
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
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SOFTWARE: Microsoft Office 97
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APPLICANT: Anderson, Shawn
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                                                                                                                                                                                                                                                                                                                          TCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTTTGAGCGAAGGCT
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                                                                                                                                                                                       12;
                                                                                                                                       Length 1697;
                                                                                                                                       ; DB 4; I
9.8e-112;
                                                                                                                                                                                    0; Mismatches 455;
                                                                                                                                          Score 383;
                                                                                                                                                               Pred. No.
                                                                                                                                       20.8%;
                                                                                                                                                                                       Conservative
                                                                                                                                                          Best Local Similarity
Matches 698; Conserv
                                             ; TYPE: DNA
; ORGANISM: Glycine
US-09-346-408-5
SEQ ID NO 5
LENGIH: 1697
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-GGAAAGTGGGGACTGGCTGGTTGGTGGAGACCTTCAGGTGCTGGAGAAAATAAGATGAGA 	IGTIGATGCAGAGGCAGAGCCAGAGCCGAGCCCAGAGCCGCCAGGCCCCCC	TACTACACCCTCTGGGCGGCTGGACCAAGGATGACGATGGCCTCTAGACTGGCGGGTGG	TCTITCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCC	CTGAAACCAAGAAGGATCTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGGCCC	AAGCCATGGACTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTCATCTCAGGAACTC	108-3 3. Application US/09346408B 5. 6338966 NFORMATION: THE Allen, Steve TH: Anderson, Shawn TH: Palco, Carl TH: Rafalski, Antoni TRYENTON: Genes Encoding Sulfate Assimilation TERENCE: BB-1167-A APPLICATION NUMBER: US/09/346,408B FILING DATE: 1999-07-01 APPLICATION NUMBER: 60/092,833 FILING DATE: July 14, 1998 FEQ ID NOS: 12 FEG ID NOS: 13
1080 590 1139 650	7 2	1319 830 1379 890	1439 950 1499 1010	1559 1070 1619 1130	1679 1190 1739 1250 1799	44 ence ence ence ence ence ence ence en
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                                                                                                                                                               778 TTGAGCGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAG 837
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                                                                                                                                   302 GAGGCCTTATCCTTGCCCAGAATCGAGCTCTCCAGCATCGATATCCAGTGGGTTCATGTG 361
                                                                                                                                                                                                                                                                                   ATTGTACTGCCCGTCTCTGCAGAGATAAGACACGGCTGGAAGGGTGCAGCAAGTTTGTC 951
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                                                                           12; Gaps
                                              Length 2280;
                                            Score 368; DB 4; Length 228
Pred. No. 7.2e-107;
0; Mismatches 435; Indels
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US-09-346-408-3
                                            Query Match 19.9%;
Best Local Similarity 60.0%;
Matches 671; Conservative
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APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
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ILING DATE: 1997-08-22
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                                                                          FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
                                                                                                                                                                                                                   APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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ILING DATE: 1997-08-22
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PPLICATION NUMBER: 60/056,878
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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  60/047,596
                                                 60/047,612
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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                                                                          1262 GATAAAACTCAGGGCAAAATGGCCTTTTTCGATCCCTCGAGACCTCAGGATTTCCTTTTC 1321
                                                                                                                                                                            1786 ATGGCCCCCAAAGCATGGAAGGTCCTGACAGATTATTA 1823
                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
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180 TGCCCTGGAGGAGTACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAA 239
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                                                                        1 TGATGGTCTAGATCAGTATCGCCTGTCTCCCAGCACACCTGCGTGAAGAGTTTGCCAGGCG
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APPLICANT: Falco, Carl
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TILE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
FURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT PILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: 60/092,833
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Pred. No. 7e-53;
0; Mismatches 162;
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Patent No. 6338966
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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Best Local Similarity 65.6%;
Matches 320; Conservative
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                                                     60/056,845
                                                                   FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/061,060
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LING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,593
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APPLICATION NUMBER: 60/056,632
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/057,650
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                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
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                                 1997-08-23
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181 GCTCCATCCACTGGGAGGATTCACAAAAGCAGATGATGTGGCCTCTTAGTTGGAGAATGAA 240

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304 CGGATTGCTGAGGTGGCTAAGCTGTTTGCTGATGCTGGTCTGGTCTGCATTACCAGCTTT 363
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                                                                                                                                                                                                                                                                                                                                    CCATTCTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGACGTAAAA
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                                    GGATGTACCGTGTGGCTAACAGGTCTCTCTGGTGCTGGAAAAACAACGATAAGTTTTGCC
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APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 TGTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTAC 649
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/346,408B CURRENT FILING DATE: 1999-07-01 EARLIER APPLICATION NUMBER: 60/092,833 EARLIER FILING DATE: July 14, 1998 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-346-408-9; Sequence 9, Application US/09346408B; Patent No. 6338966
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   Conservative
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APPLICANT: Allen, Steve
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method of producing a composite fermented beverage using genetically modified yeast
                                                    1499
                                                                                                                    1500 GATGATTGCGGGTGCCAATTTCTACATTGTGGGGAGGGACCCTGCAGGAATGCCCCATCC 1559
                                                                                                                                                                                         .560 TGAAACCAAGAAGGATCTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGGCCCC 1619
                                                                      1440 CTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCG
                                                                                                                                         Score 169.2; DB 4; Length 1160; Pred. No. 1.1e-43;
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/09/153,310
FILING DATE: 15-Sep-1998
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear MOLECULE TYPE: Genomic DNA; SEQUENCE DESCRIPTION: SEQ ID NO: 41: US-09-153-310-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hansen, Jorgen
Johannesen, Pia Francke
Pedersen, Mogens Bohl
Sorensen, Steen Bech
F INVENTION: Method of produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNET/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION UNMBER: 29,768
REFERENCE/DOCKET NUMBER: <U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-672-5300
TELEFAX: 202-672-5399
                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09153310 Patent No. 6326184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gjermansen, Claes
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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                            TGTGGCTAACAGGTCTCTCTGGTGCTGGAAAAACAACGATAAGTTTTGCCCTGGAGGAGT 193
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                                                         104 IAIGGITIACAGGGCIAICIGGGICAGGGAAAICAACGGICICIGIIGCCIIAGAAAAG
                                                                                         ACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCATGGCC
                                                                                                                                                                                                                                                       284 AAGTAGCAAAATTAATGGTAGACGCTGGAGCCTTAAACAGTTACTGCTTTTATCTCCCCAT
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, John C.
APPLICANT: VENTER, JOHN C.
CURRENT FILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
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Pred. No. 1.5e-22;
); Mismatches 250; Indels 0;
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OTHER INFORMATION: H37Rv
US-09-103-840A-1
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SEQ ID NO 1
LENGTH: 4411529
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Best Local Similarity
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US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1266 GCAGGACACCTGCCGCAGGCTCCTAGAGAGGGGCTACAAGCACCCGGTCCTCCTACTACA 1325
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Pred. No. 1.6e-35;
0; Mismatches 111; Indels
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Best Local Similarity 66.39
Matches 220; Conservative
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Best Local Similarity
Matches 274; Conserva
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US-09-346-408-9
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LOCATION:
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LOCATION:
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FEATURE:
NAME/KEY:
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1439842 TGGGCTTTTCCATGGCCGACCGCGGAGAACCTGCGCCGGCTGTCGCATGTGGCCACA 1439901
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                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGGAGATTAAAAGGATTTACAGGTATTGATTCTGATTATGAGAAACCTGAAACTCCTG
                                                                  TGTTTGCTGATGCTGGTCTGGTCTGCATTACCAGCTTTATTTCTCCATTCGCAAAGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGTGTGCTTAAAACCAATTTGTCCACAG 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.6;
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APPLICATION NUMBER: EP 91 114 300.
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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1800 Diagonal Road,
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INFORMATION FOR SEQ ID NO: 14:
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      ATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCATGCCCTTAACAGAAATC 265
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COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
GS-09-103-840A-2
                                                         1440313 AGGGCATCTCCGCTTACGTTCTGGACGGCGACAACCTACGGCATGGCCTCAACGCCGACC
                                                                                                               TCGGATTCTCCTGGGGACAGAGGGAAAATATCCGCCGGATTGCTGAGGTGGCTAAGC
                                                                                                                                                                                                                                  TGTTTGCTGATGCTGGTCTGGTCTGCATTACCAGCTTTATTTCTCCATTCGCAAAGGATC
                                                                                                                                                                                                                                                                                                                                               386 GTGAGAATGCCCGCAAAATACATGAATCAGCAGGGCTGCCATTCTTTGAAATATTTGTAG
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 4.9e-22;
0; Mismatches 251
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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Matches 259; Conserv
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LENGTH: 4403765
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1120 CTGGAGAAAATAAGATGATGATGGCCTGGACCAATACCGTCTGACACCTCTGGAGCTC 1179
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                                                                                    140 SRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNR 199
             80 SRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNR 139
                                                                                                                                                                      200 SRNRNRSRNRNRSRRRNRNSRCRARGRCRURGRCRGRURARARCRURCRURURGRCRGRCR 259
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09244796
Fatent No. 6281344
GENERAL INFORMATION:
APPLICANT: SZOSCAK, Jack W.
APPLICANT: SZOSCAK, Jack W.
APPLICANT: SZOSCAK, Jack W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: 05/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER PRILICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FSSESSO for Windows Version 4.0
LENGTH: 289
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10.3%; Pred. No. 0.53;
Live 95; Mismatches 141;
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; other information: n = A,T,C or G
US-09-244-796-17
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Best Local Similarity 10.3%
Matches 27; Conservative
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                                                                                                                                                                                                                                             914 AGGATAAGACACGGCTGGAAGGGTGCAGCAAGTTTGTCCTGGCACATGGTGGACGAGGG
                                                                                                                                                         854 CCCTGCTAGATGATGCGTGATCAACATGAGCATCCCCATTGTACTGCCCGTCTCTGCAG
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APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
                             Indels
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5.4%; Pred. No. 0.00044; ative 214; Mismatches 173;
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Best Local Similarity 10.3%; Pred. No. 0.53;
Matches 27; Conservative 95; Mismatches 141;
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CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(289)
COTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
Best Local Similarity 5.4%; Pred
Matches 22; Conservative 214;
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US-09-007-005-17
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Sequence 81, Appl
Sequence 1680, Ap
Sequence 1680, Appl
Sequence 160, Appl
Sequence 2167, Ap
Sequence 255, Appl
Sequence 1752, Appl
Sequence 1753, Appl
Sequence 1754, Appl
Sequence 574, Appl
Sequence 574, Appl
Sequence 574, Appl
                               Sequence 1736, App
Sequence 377, App
Sequence 710, App
Sequence 264, App
Sequence 6045, App
Sequence 6045, App
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 1420940CB1
US-09-974-298-183
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Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: CHER, Huel-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
SOFTWARE: PERL PROGRAM
SEQ ID NO 183.
LENGTH: 2617
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               US-09-974-300-2074
US-09-974-300-2074
US-09-88-574-1736
US-09-74-1669-264
US-09-70-988-1
US-09-70-988-1
US-09-70-988-1
US-09-771-161A-62
US-09-771-161A-62
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US-09-771-161A-62
US-09-771-161A-62
US-09-771-161A-62
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US-09-736-457-1752

US-09-902-941-1752

US-09-849-626-1752

US-10-017-754-1752

US-10-123-155-10

US-10-123-155-234
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US-09-878-574-2555
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US-10-184-634-574
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.0%;
Matches 1841; Conservative
    283
594
365
548
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265
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368
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311
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    8.6
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94.2
93.4
92.4
85.4
82.2
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Sequence 86, Appl
Sequence 116, App
Sequence 116, App
Sequence 2084, Ap
Sequence 8898, Ap
Sequence 8898, Ap
Sequence 12859, Ap
Sequence 12859, Ap
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
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23146, A
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Sequence 86, Appl
Sequence 116, App
                                                                                                                       (without alignments)
8934.763 Million cell updates/sec
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Seguence 2314
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                                                                                                     June 4, 2003, 16:43:32; Search time 289 Seconds
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/ptodata/2/pubpna/USOG_NEW_PUB.seq:*/
/ptodata/2/pubpna/USOG_PUBCOMB.seq:*/
/ptodata/2/pubpna/OSO7_NEW_PUB.seq:*/
/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*/
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-864-761-6431
US-09-864-761-23146
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US-09-938-842A-2084
US-09-880-107-360
US-09-796-692-8898
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US-10-198-846-5659
US-10-198-846-12859
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PRIOR APPLICATION NUMBER: US 60/048,186
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; ORGANISM: Homo sapiens
US-09-984-245-86
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Matches 1305; Conserv
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larity 71.3%; Pred. No. 0;
Conservative 0; Mismatches
           US 60/054,804
                       PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 116
LENGTH: 2527
           APPLICATION NUMBER:
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Best Local Similarity
Matches 1305; Conserv
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; ORGANISM: HOMC
US-09-984-245-116
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                                          1714 CACTITGGAAATAGTTCCCTTTCGAGTTGCAGCTTACAACAAGAAAAAAGAGCGTATGGA 1773
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Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
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PRIOR FILING DATE: 1998-03-19
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PRIOR PRILOR FILING DATE: 1997-03-21
PRIOR PELLICATION NUMBER: US 60/041,276
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PRIOR FILING DATE: 1997-03-21
PRIOR PELLICATION NUMBER: US 60/041,281
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PELLING DATE: 1997-05-30
PRIOR PELLICATION NUMBER: US 60/048, 185
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PRIOR PELLICATION NUMBER: US 60/048, 186
PRIOR PELLICATIO
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US20030050461A1

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APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
                                                                                                                               PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR FLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
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APPLICATION NUMBER: US 60/042,344
ELLING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,276
FILING DATE: 1997-03-21
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FILING DATE: 1997-03-21
PRILING DATE: 1997-03-21
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,350
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APPLICATION NUMBER: US 60/048,188
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FILING DATE: 1997-05-30
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FILLING DATE: 1997-05-30
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FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,355
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PPLICATION NUMBER: US 60/048,160
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,351
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FILING DATE: 1997-05-30
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LENGTH: 2527
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                          1089 GGACTGGCTGGTTGGTGGAGACCTTCAGGTGCTGGAGAAAATAAGATGGAATGAGCCT
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68 GATCAAGAAGCAAAAGACGGAGAACCAGCAGAAATCCACCAATGTAGTCTATCAGGCCCA Gaps = = ö Length 2527; 525; Indels DB 9; Score 990; DB Pred. No. 0; Mismatches Ouery Match 53.7%; Best Local Similarity 71.3%; Matches 1305; Conservative ; ORGANISM: Homo sapiens US-09-966-262-86

RESULT 4 US-09-966-262-86 ; Sequence 86, Application US/09966262

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APPLICATION N	QQ	394 CGCAGAAGTTGCTAAACTGTTTGCAGATGCTGGCTTAGTGTGCATCACAAGTTTCATATC 453
PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,188	Qy	369 TCCATTCGCAAAGGATCGTGAGAAAGCCCGCAAAATACATGAATCAGCAGGGCTGCCATT 428
PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,135	QQ	454 ACCTTACACTCAGGATCGCAAGGAAGGCAAATTCATGAAGGTGCAAGTTTACCGTT 513
PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/050,937 PRIOR FILING DATE: 1907-05-30	Qy	CTTTGAAATATTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGAGAG
	QQ .	TTTTGAAGTATTTGTTGATGCTCCTCTGCATGTTTGTGAACAGAGGATGTCAAAGGACT
	g G	489 CTATAAAAGGGCCAGAGCTGGGGGAGTTTAAAGGATTTACAGGTATTGATTCTGATTATGA 548 
	oy E	549 GAAACCTGAAACTCCTGAGCGTGTGCTTAAAACCAATTTGTCCACAGTGAGTG
PRIOR APPLICATION NUMBER: US 60/048,069 PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,065	Qy	CCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCCTATACTATAATCAAAGA
FILING DATE: 1997-0 APPLICATION NUMBER:	qa	694 CCAGCAAGTTGTGGAACTTCTACAGGAACGGGATATTGTACCTGTGGATGCATGTATGA 753
PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,096 PRIOR FILING DATE: 1997-05-30	Qy	669 TATCCACGAACTCTTTGTGCCGGAAAACAAACTTGACCACGTCCGAGCTGAGGCTGAAAC 728 
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PRIOR APPLICATION NUMBER: US 60/048,351 PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/048,154	Oy	CTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGGAGTACTTACAGGTTATGCACTT
PRIOR APPLICATION NUMBER: US 60/054,804 PRIOR FILING DATE: 1997-08-05 PRIOR FILING DATE: 1997-08-19 PRIOR FILING DATE: 1997-08-19	g V d	8/4 TTGGGCAACCCCATTGAATGGCTTTATGAGAGAGGGAGTACTTGCAGTGCCTTCATTT 933 849 TGACACCCTGCTAGATGGCGTGATCAACATGAGCATCCCCATTGTACTGCCGTCTC 908 1
PRIOR APPLICATION NUMBER: US 60/060,862 PRIOR FILING DATE: 1997-10-02 NUMBER OF SEQ ID NOS: 343 SOFTWARE: Patentin Ver. 2.0	Qy	TGCAGAGGATAAGACACGCTGGAAGGTGCAGCAACTTTGTCCTGGCACATGGTGGACG TGTAGAAGATAAAGAGAGCTGGACGGCTGTACAGCAATTGCTCTGATGAGGCCGCTGAAGGTTAGAGGCCGCTGTACAGCAATTGCTCTGATGAGGCCG
SEQ ID NO 116 SEQ TO NO 116 TYPE: DNA ORGANISM: Homo sapiens	Qy	GAGGGTAGCTATACGAGACGTGAATTCTATGAACACAGAAAAGGGAACGCTGTTC -
53.7%; Score 990; DB 9; Length 2527; Similarity 71.3%; Pred. No. 0;	Qy	1029 CCGTGTTTGGGGGACAACATGTACAAAACACCCCCATATCAAAATGGTGATGGAAAGTGG 1088
SCHANAGACGAGAAATCCACCAATGTAGTCTATCAGGCCCA	QY Db	1089 GGACTGGCTGGTGGAGACCTTCAGGTGCAGAAAAAAAAAGATGGAATGATGGGCT 1148 
	Qy	1149 GGACCAATACCGTCTGGAGCTCAAACAGAAATGTAAAGAAATGAATG
	Qy Db	1209 IGCGGIGTITGCATTCCAGTIGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCA 1268 HH H H H H H H H H H H H H H H H H H H
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TGGCCTTAACAGAAATCTCGGATTCTCCTGGGGACAGAGGAAAATATCCGCGGT	Qy Db	1329 TCTGGGCGGCTGGACCAAGGATGACGATGTGCCTCTAGACTGCGGATGAAGCAGCACGC 1388
33* AGGICLOMAIMMANDICTIONCTITANTICTIONANGACAGAGAGAGAGAGATGTICGACGCAT 393 309 TGCTGAGGTGGCTAAQCTGTTTGCTGATGCTGGTCTGGTTGCATTACTTC 368	Qy	1389 GGCTGTGCTCGAAGGGGTCCTGGATCCCAAGTCAACCATTGTTGCCATCTTTCCGTC 1448

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Pred. No. 0;
0; Mismatches 525;
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR PLING DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: US 60/048,355
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PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
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71.3%;
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ORGANISM: Homo sapiens
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                        TCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCGGATGATTGC
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
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PRIOR APPLICATION NUMBER: US/09/983,966
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PRIOR FILING DATE: 1998-09-17
PRIOR FLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-09-19
PRIOR PLICATION NUMBER: PCT/US98/05311
PRIOR PLICATION NUMBER: US 60/041,277
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PRIOR PLICATION NUMBER: US 60/041,277
PRIOR PLING DATE: 1997-03-21
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694 CCAGCAAGTIGTGGAACTTCTACAGGAACGGGATATTGTACCTGTGGATGCATCTTATGA 753 669 TATCCACGAACTCTTGTGCCGGAAAACAAACTTGACCAGGTCCGAGGTGAGGCTGAAAC 728	789 CTGGGCCACTCCCTCAAAGGTTTCATGCGGAGAAGGAGTACTTACAGGTTATGCACTT 848  [   1   1   1   1   1   1   1   1   1	909 TGCAGAGGATAAGACACGGCTGCAAGCTTTGTCCTGGCACTGGTGGCG 968	1029 CCGTGTTTGGGGGACAACATGTACAAAACACCCCCATATCAAAATGGTGATGGAAAGTGG 1088	1149 GGACCAATACCGTCTGACACCTCTGGAGCTCAAACAGAAATGTAAAGAATGAAT	1269 GGACACCTGCCGCGGGGCTCTAGAGGGGCTACAAGCACCCGGTCCTCCTACTACACCC 1328	GGCTGTGCTCGAAGGGGTCCTGGATCCCAAGTCAACCATGTTGCCATCTTTCCGTC 144	1599 AGGACCAACTTTTTACATTGTGGGAGGGCCCTGCAGGAATGCCCCATCCTGAAACCAA 1568 16111111111111111111111111111111111
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                          GAGGGTAGCTATCTTACGAGACGCTGAATTCTATGAACACAGAAAAGGGAACGCTGTTC
                                                 CCGTGTGGCCATTCTTCGCAATCCAGAGTTTTTTGAGCACAGGAAAGAGGAGCGCTGTGC
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Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Prot
FILE REPERENCE: PS004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
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; Sequence 116, Application US/10143090
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; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2527
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71.3%;
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Best Local Similarity 71.3
Matches 1305; Conservative
                                                     TYPE: DNA
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                                                                                                                           Length 2527;
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                                                                                                                          Score 990; DB Pred. No. 0; Mismatches
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                            ;
                                                                                                                         53.7%;
llarity 71.3%;
Conservative
                                                                                              ; ORGANISM: Homo sapiens US-10-143-090-116
                                                                                                                                   Similarity
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Best Local Simil
Matches 1305; (
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                          1564 ACCAAGAAGGATCTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGGCCCTGGC
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Pred. No. 2.9e-96;
0; Mismatches 148; Indels
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APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liv
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1804 AAGGTCCTGACAGATTATTAC 1824
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Patent No. US20020142981A1
GENERAL INFORMATION:
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al Similarity 73.9%;
424; Conservative
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LOCATION: (1)..(574)

OTHER INFORMATION: n

US-09-880-107-360
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Best Local Similarity
Matches 424; Conserv
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LENGTH: 574
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                                                                      PLANTS CONTAINING
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                  APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, TOOL
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLAN
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
SEQ ID NO 2084
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1436 CCATCTTTCCGTCTCCCATGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGT 1495
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NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8898
LENGTH: 600
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R FILING DATE: 2000-04-27

NR APPLICATION NUMBER: US 60/200,303

NR FILING DATE: 2000-04-28

NR APPLICATION NUMBER: US 60/200,779

NR FILING DATE: 2000-04-28

NR FILING DATE: 2000-05-01
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CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
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                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (572)
; OTHER INFORMATION: n=A,T,C or
US-09-796-692-8898
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75.2%;
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                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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APPLICANT: Adgate, Paul A.
APPLICANT: Adgate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: DO1200
CURRENT APPLICATION NUMBER: 00/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
1215 GTTTGCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCAGGACAC 1274
                                                                                                                                                                                                                                                                                     1335 CGCTGGACCAAGGATGACGATGTGCCTCTAGACTGGCGGATG-AAGCAGCACGCGGGTG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                   1394 IGCICGAGGAAGGGGICCIGGAICCCAAGICAACCATIGIIGCCAICIIICCGICICCCA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 TGTTATATGCTGGCCCCACAGAGGTCCAGTGGCACTGCAGGTCCCGGATGATTGCGGGTG 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAATITICIACATIGIGGGGGGGGCCCTGCAGGAATGCCCCATCCTGAAACCAAGAAGG 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1574 ATCTGTATGAACCCACTCATGGGGCAAGGTCTTGAGCATGGCCCCTGGCCTCACCTCTG 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1634 TGGAAATCATTCCATTCCGAGTGGCTGCCTACAACAAAGCCAAAAAAGCCATGGACTTCT 1693
                                                                                                                                                                                                                                                                                                                                 395 TGGCTGGACAAAGGATGACGATGTTCCTTTGATGTGGCGTATGAAGCAGCATGCTGCAG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 CCAACTITIACATIGITIGGACGAGACCTGCTGGCATGCCTCATCCAGAAACAGGGAAGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1275 CTGCCGCAGGCTCCTAGAGAGGGGCTACAAGCACCCGGTCCTCCTACTACACCCTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 CTTTGCATTTCAACTACGCACCCCAGTGCACAATGGACATGCCCTGTTAATGCAGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1694 ATGATCCAGCAAGGCACAATGAGTTTGACTTCAT 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8898, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR PELICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
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APPLICATION NUMBER: 60/223,378
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1535 GGGACCCTGCAGGAATGCCCCATCCTGAAACCAAGAAGGATCTGTATGAACCCACTCATG 1594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GGGGCAAGGTCTTGAGCATGGCCCTGGCCTCACTGTGGAAATCÄTTCCATTCCGAG 306
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wongyao
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
SOFTWARE: FASEEQ for Windows Version 4.0
SEQ ID NO 12859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1475 AGGTCCAGTGCCACTGCAGGTCCCGGATGATTGCGGGTGCCAATTTCTACATTGTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGCAAGGTCTTGAGCATGGCCCCTGGCCTCACCTCTGTGGAAATCATTCCATTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1655 TGGCTGCCTACAACAAAGCCAAAAAAGCCATGGACTTCTATGATCCAGCAAGGCA 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 803;
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                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: 620, 658, 687, 703, 727, 754, 764, 765, 783, 792
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-5659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 2.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 233.4; DB 9;
Pred. No. 2.4e-68;
0; Mismatches 1;
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                         PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12859, Application US/10198846 Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8,
LOCATION: 18, 19, 824, 825, 826
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12859
       2002-07-18
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99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 12.7%;
al Similarity 99.6%;
234; Conservative
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                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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US-10-198-846-12859
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Best Local
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Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1556 ATCCTGAAACCAAGAAGGATCTGTATGAACCCACTCATGGGGGCAAGGTCTTGAGCATGG 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1616 CCCCTGGCCTCACCTCTGTGGAAATCATTCCATTCCGAGTGGCTGCCTACAACAAAGCCA 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1676 AAAAAGCCATGGACTTCTATGATCCAGCAAGGCACAATGAGTTTGACTTCATCTCAGGAA 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICGAATGAGGAAGCICGCCCGGGAAGGAGAATCCCCCAGAIGGCTTCATGGCCCCCA 1795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1796 AAGCATGGAAGGTCCTGACAGATTATTACAGGTCCCTGGAGAA 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 243; DB 9; Length 60 75.2%; Pred. No. 1.1e-71; Live 0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR PILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SEQ ID NO 8898
LENGTH: 600
                                                                                                  PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
APPLICATION NUMBER: US 60/202,084
                                FILING DATE: 2000-05-04 APPLICATION NUMBER: US 60/206,201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (572)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.28
Best Local Similarity 75.28
Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lillie, James APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (572)
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US-10-198-846-5659
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1535   GGGACCCTGCAGGAATGCCCCATCCTGAAACCAAGAAGGATCTGTATGAACCCACTCATG   1594
Oy 1535 GGGAG OD 431 GGGAG OY 1595 GGGGC OY 1695 GGGGC OY 1655 TGGCT OY 1655 TGGCT OD 551 TGGCT OD 551 TGGCT

757.2 41.0 860 13 BIB31135 743.6 40.3 949 14 BQ926758 734.8 39.8 1041 13 BIB29344 722.6 39.2 1054 14 BQ942867 704.8 38.2 874 14 BQ942867 672.4 36.4 917 14 BQ943947 629 34.1 683 12 BG484421 624 8 33.9 650 12 BE786139 624 33.8 797 13 B1103516 613 8 33.3 620 13 BM263737	582.8 31.6 1048 14 BM903600 580.4 31.5 873 14 BQ221395 579.4 31.4 684 12 BQ438005 558.8 30.3 767 9 AIG48997 546.8 29.6 972 14 BQ896549 517.8 28.6 640 12 BG823104 517.8 28.1 959 9 AIS74314 513.2 27.8 624 10 BF182876 512 27.8 624 10 BE292722	508 27.5 944 13 BM458625 503 27.3 946 12 BG490797 488.8 26.5 492 14 BM708017 476.8 25.2 584 12 BG723809 459 24.9 576 10 BB311856 441.4 23.9 870 13 B1338434 436.2 23.6 557 10 AW571670	35 433.8 23.5 741 13 B1855664 B1855664 603383187 36 425.8 23.1 709 14 BQ571984 B66571984 UT-M-FB0- 37 425.2 23.0 886 14 BQ552788 B6655788 AGENCOURT 38 424.4 23.0 712 12 BG778039 BG778039 60265432 40 423.6 23.0 1062 12 BG778039 BG778039 60265432 41 419.2 22.7 979 13 B1257912 BG116418 B61257912 602970843 42 417.6 22.6 711 13 B1642947 B1649417 603277863 43 415.6 22.5 804 13 B1852668 B1852968 603379782 44 412.8 22.4 715 13 B1081933 AL517203 AL517203 ALGINMENTS	RESULT 1 B0957456 LOCUS LOCUS DEFINITION AGENCUNT-8786574 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:6371441 ACCESSION SOFF456 VERSION B0957456 IG:22372934 KEYWORDS SOURCE Numan. ORGANISM Homo sapiens BURATYOta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; REFERENCE 1 (Dases 1 to 956)	AUTHORS NIH-WGC http://mgc.nci.nih.gov/.  TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)  COMMENT Contact: Robert Strausberg, Ph.D. Email: Gapbbs-rémail.nih.gov Tissue Procurement: DCTD/PTMF/Gazdar CDNA Library Preparation: Rubin Laboratory CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2945 row: j column: 18 High quality sequence stop: 633.  FEATURES Location/Qualifiers
GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: June 4, 2003, 15:10:31; Search time 2709 Seconds (without alignments) (without alignments) (without alignments)	Title: US-09-898-165B-9 Perfect score: 1845 Sequence: 1 atgtcggggatcaagaagcaggtccctggagaagaactaa 1845 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 16154066 seqs, 8097743376 residues	mber of hits satisfying chosen par DB seq length: 0 DB seq length: 2000000000 cessing: Minimum Match 0% Listing first 45 summarie	Database : EST:*  1: em_estba:* 2: em_estbin:* 3: em_estmin:* 4: em_estmin:* 5: em_estpi:* 6: em_estpi:* 7: em_estro:* 8: em_htc:* 9: gp_est:* 11: gp_htc:* 12: gp_est:* 13: gp_est:* 13: gp_est:*	14: gb_est5:*  15: em_estfun:*  16: em_estfun:*  17: gb_gss:*  18: em_gss_lnum:*  20: em_gss_ln:*  21: em_gss_pin:*  22: em_gss_pin:*  23: em_gss_mam:*  24: em_gss_mam:*  25: em_gss_mam:*  26: em_gss_pin:*  27: em_gss_pin:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.           Result         SUMMARIES           Result         Core Match Length DB ID         Description           1         907         49.2         956         49.1         1766         11         BC032513         AL540583         AL540583         AL540583         AL540583         AL550460         AL550460         BQ924373         BQ924373         AGBNCOURT         BQ9220909         AGBNCOURT         BQ220909         AGBNCOURT

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ACTACACCCTCTGG-GCGCCTGGACCAAGGATGACGATGTGCCCTCTAGACTGGCGGATGA 1378
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Contact: nisc_mg@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Mos.E.L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogf,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                    840
                                                                                                                                                                                                                                                                                                                                  27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G. B. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 69 Row: e Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127474
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-JUN-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                             1379 AGCAGCACGCG-GCTGTGCTCGAGGAGGGGTCCTGGATCCCAAGTCAACCATTGT 1433
                                                                                                                    1260 GTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGGGCTACAAGCACCCGGTCCTCCT
                                                                                                                                                                                                                                                                                                                         BC032513 1766 bp mRNA linear HTC 27-JUN.
Homo sapiens, Similar to 3'-phosphoadenosine 5'-phosphosulfate
Synthase 1, clone IMAGE:5492659, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) MAS Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                         Length 1766;
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.4e-255;
es 479; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nc1.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5492659"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
366 c 476 g 438 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 905.6; Pred. No. 8.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              GI:21619118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.1%;
Best Local Similarity 71.4%;
Matches 1193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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BC032513.1
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                                                                                                                                                                                                                                                                                    RESULT 2
BC032513
                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
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COMMENT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:6371441"
/clone="INAGE:6371441"
/clone=Lib="NIH_MGG:18"
/tissue_type="large cell carcinoma"
/tlab_host="All108 (phage-resistant)"
/lab_host="All108 (phage-resistant)"
/note="Organ: lung; Vector: poTBF; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRiX/AnoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTGGACGGAGGGTAGCTATCTTACGAGACGCTGAATTCTATGAACACAGAAAAGAGGA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCTGTTCCCGTGTTTGGGGGACAACATGTACAAAACACCCCCATATCAAAATGGTGAT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAAGTGGGGACTGGCTGGTGGAGACCTTCAGGTGCTGGAGAAATAAGATGGAA 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AAAAGGCCTCTATAAAAGGGCCAGAGCTGGGGAGATTAAAAGGATTTACAGGTATTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATTATGAGAAACCTGAAACTCCTGAGCGTGTGCTTAAAAACCAATTTGTCCACAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840 TATGCACTTTGACACCCTGCTAGATGATGGCGTGATCAACATGAGCATCCCCATTGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCGTCTCTGCAGAGGATAAGACACGGCTGGAAGGGTGCAGCAAGTTTGTCCTGGCACA
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                                                                                                                                                                                                                                                                                                                                                              Score 907; DB 14;
Pred. No. 2.4e-255;
0; Mismatches 16;
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98.18;
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Best Local Similarity 98.1
Matches 938; Conservative
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Οy	9 GATCAAGAAGCAAAAGGGGAGAAACCAGCAGAAATCCACCAATGTAGTCTATCAGGCCCA 68	Qy	1089 GGACTGG(
qq		qq	1172 AGATTGG
Qy	69 CCATGTGAGGAGGAATAAGAGGGGCAAGTGGTTGGAACAAGGGGTGGGT		
qa	152 TCATGTCAGCAGGAACAAGAGAGGTCAGGTGGTGGGACCAGAGGTGGCTTTCGTGGTTG 211	qa	
οy	129 TACCGTGTGGCTAACAGGTCTCTCTGGTGCTGGAAAACAACGATAAGTTTTGCCCTGGA 188	Oy 4	
qa	212 CACAGTTTGGCTAACAGGCTTGTGTGTGTGTGTGTGTGTG	a :	
ΟŊ	189 GGAGTACCTTGTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCA 248	ζ, d	1209 GGACACC
QQ	272 GGAGTACCTGGTTTGTCATGGTATTCCATGCTACACTCTGGATGGTGACAATATTCGTCA 331		
Óλ			
qq	332 AGGTCTCAATAAAATCTTGGCTTTAGTCCTGAAGACAGAGAGAAGAGATGTTCGACGCAT 391		1 0
Qy	309 TGCTGAGGTGGCTAAGCTGTTTGCTGATGCTGGTCTGCATTACCAGCTTTATTC 368		
qa	392 CGCAGAAGTTGCTAAACTGTTTGCAGATGCTGGCTTAGTGTGCATCACAAGTTTCATATC 451		
Oy	369 TCCATTCGCAAAGGATCGTGAGAATGCCCGCAAAATACATGAATCAGCAGGGCTGCCATT 428		
qa	452 ACCTTACACTCAGGATCGCAACAATGCAAGGCAAATTCATGAAGGTGCAAGTTTACCGTT 511		
QY	429 CTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGACGTAAAAGGCCT 488		
qa	512 TTTGAAGTATTTGTTGATGCTCCTCTGCATGTTTGTGAACAGAGGGATGTCAAAGGACT 571		
Qy	489 CTATAAAAGGGCCAGAGCTGGGGAGTTAAAAGGATTTACAGGTATTGATTCTGATTATGA 548		1569 GAAGGATC
qa	572 CTACAAAAAGCCCGGCAGGAGAAATTAAAGGTTTCACTGGGATCGATTCTGAATATGA 631		1652 GAAGGATG
Qy	549 GAAACCTGAAACTCCTGAGCGTGCTTAAAACCAATTTGTCCACAGTGAGTG		1429 CTCTGTG
QQ	632 AAAGCCAGAGGCCCCTGAGTTGGTGCTGAAACAGACTCCTGTGATGTAAATGACTGTGT 691	gg	1712 CACTTIG
δλ	609 CCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCCTATACTATAATCAAAGA 668	RESULT 3	
ପ୍ଧ	AAGTIGTGGAACTICTACAGGAACGGGAT	LOCUS	AL540583
ον	669 TATCCACGAACTCTTTGTGCCGGAAAACAAACTTGACCACGTCCGAGCTGAGGCTGAAAC 728	NOTSSAUDA	
qq	aigigccagaaataaacticattiggcaaaac	VERSION VERSION	AL540583.1
. QY	729 TCTCCCTTCATTATCAATTACTAAGCTGGATCCCAGGTCCAGGTTTTGAGCGAAGG 788	SOURCE	
qa	812 ATTACCAGCACTGAAAATTAATAAAGTGGATATGCAGTGGGTGCAGGTTTTGGCAGAAGG 871	GINGONO	Eukaryota;
Qy	789 CTGGGCCACTCCCTCAAAGGTTTCATGCGGAGAAGGAGTACTTACAGGTTATGCACTT 848	REFERENCE	
qq	ATTGAATGGCTTTATGAGAGAGAG	TITLE	
δλ	849 TGACACCCTGCTAGATGATGGCGTGATCAACATGAGCATCCCCATTGTACTGCCGTCTC 908	COMMENT	
qa	932 TGATTGTCTTCTGGATGGAGGTGTCATTAACTTGTCAGTACCTATAGTTCTGAGGTCTGCGAC 991		Genoscope BP 191 91(
Qy	909 TGCAGAGGATAAGACACGGCTGGAAGGGTGCAGGTTTGTCCTGGCACATGGTGGACG 968	FEATURES	
qa	992 TCATGAAGATAAAGAGAGGCTGGACGCTGTACAGCATTTGCTCTGATGTATGAGGGCCG 1051	500	,
Oy.	969 GAGGGTAGCTATCGGAGACGCTGAATTCTATGAACACAGAAAAGGGGAACGCTGTTC 1028		
qq	1052 CCGTGTGGCCATTCTTCGCAATÇCAGAGTTTTTGAGCACAGGAAAGAGGAGCGCTGTGC 1111		
oy 1	CCGTGTTTGGGGGACAACATGTACAAAACACCCCCATATCAAAATGGTGATGGAAAGTGG		.00
Q	IIIZ CAGACAGTGGGGAACGACATGCAAGAACCACCCTATATTAAGATGGTGATGGAACAAG 1171		(C 124

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951 bp mRNA linear EST 16-FEB-2001 LTL_FL002_PL1 Homo sapiens CDNA clone CS0DE002YM23 5 prime equence.
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                    STITCCATTCCAGTTGCGCAATCCTGTCCACAATGGCCATGCCCTGTTGATGCA 1268
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; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       TIGCCGCAGGCTCCTAGAGGGGGCTACAAGCACCCGGTCCTCCTACTACACCC
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1006 EVRY cedex - France
eqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Gruber,C., Jessee,J. and Polayes,D.
gth cDNA libraries and normalization
hed (2001)
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Technologies. Contact: Feng Liang Life Technologies, a distain of Invitrogen 9800 Medical Center Drive Rockville (Maryland 20860, USA, Fax: (1) 301 610 8371 Email: filang@lifetech.com URL:
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                                        2 others
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                               http://fulllength.invitrogen.com"
231 c 245 g 227 t
                                                                Score 866.2; DB 9;
Pred. No. 2.5e-243;
; Mismatches 0;
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/clone="tsollo577002"
/cloned with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL: http://fullength.invitrogen.com"

43 a 200 c 227 g 214 t 2 others
                             bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CSODIO57YO02 5
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Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web.: www.genoscope.cns.fr.
Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 99.9%; Pred. No. 6.2e-240;
4; Conservative 1; Mismatches 0;
                             886
Homo
                                            LTI_NFL006_PL2
                                                                                        AL550460.1 GI:12887457
                                                          prime, mRNA sequence.
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Db 4		BASE COUNT	Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 252 a 210 c 245 g 207 t 1 others
r vo	AAAGGCCTCTATAAAAGGGCCAGAGCTGGGGAGATTAAAGGATTTACAGGTATTCT AAAGGCCTCTATAAAAGGGCCAGAGCTGGGGAGATTAAAGGGATTTACAGGTATTCT	ORIGIN Query Ma	۽ ب
N N	541 GATTATGAGAAACCTGAAACTCCTGAGCGTGTGCTTAAAACCAATTTGTCCACAGTGAGT 600 	Matc	895
99	601 GACTGTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCCTATACTATA 660 	QQ OA	
. 0	ATCAAGGTATCCACGGACTCTTTGTGCCGGAAACAAACTTGACCAGGTCCGGGCTGAG	7 dd	
9 1	ATCHART CARCAN CONTROLL OF THE CONTROLL OF T	λο 1	TGTCCACAGTGAGTGACTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTG
, ,	/21 GCTGAACTCTCCCTCATTATCAATGCTGGATCTCCAGTGGGTCCAGGTTTTG 780 	Q O	121 TGTCCACAGTGAGTGACTGTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATG 180 647 TACCCTATACTATAATCAAGATATCCACGAACTCTTTGTGCCGGAAACAAAAAAACAAAC
7	AGCGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGAGTACTTAC?	qa	181 TACCCTATACTATATCAAAGATATCCACGAACTCTTTGTGCCGGAAACAAAC
<b>&amp;</b> &	805 AGCGARGGTGGGCCACTCCCTCAAAGGTTTCATGCGGAGAAGGAGTACTTACAGGTT 864 841 ATGCACTTTGACACC 855	QY Db	707 ACGTCCGAGCTGAGGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGT 766
	865 AIGCACTITGACACC 879	Qy	• 767 GGGTCCAGGTTTTGAGCGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGG 826
RESULT 5 BQ924373 LOCUS DEFINITION	BQ924373 91733 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374672	Qy	827 AGTACTTACAGGTTATGCACTTTGACACCCTGCTAGATGATGGGGTGATCAACATGAGCA 886
ACCESSION VERSION KEYWORDS	9. intro Sequence. B0924373.1 GI:22339404 EST.	Qy	887 TCCCCATTGTACTGCCCGTCTCTGCAGAGATAAGACACGGCTGGAAGGGTGCAGCAAGT 946 
ORGANISM	numan. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Q7 Q1	947 TTGTCCTGGCACATGGTGGACGGGTAGCTATCTACGAGACGCTGAATTCTATGAAC 1006
REFERENCE AUTHORS TITLE JOURNAL	<pre>1 (bases t to 915) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)</pre>	Qy Dp	1007 ACAGAAAAGAGGAACGCTGTTCCCGTGTTTGGGGACAACATGTACAAAACACCCCCATA 1066 
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.opp. Tissue Procurement: DCTD/DTP/Gazdar CDNA Library Preparation: Rubin Laboratory	Qy Dp	1067 TCAAAATGGTGATGGAAGTGGGGACTGGTTGGTGGAGACCTTCAGGTGCTGGAGA 1126 
	Consoling Alactic Description of the Limit of the Consoling (LENE)  Clone distribution: MGC clone distribution information can be found through the LiMiA.G.E. Consortium/LLNL at:	δγ	1127 AAATAAGATGGAATGAT-GGGCTGGACCAATACCGTCTGACACCTCTGGAGCTCAAACAG 1185 
FEATURES	nttp://lmage.iin.gov Plate: LLCM254 row: a column: 09 High quality sequence stop: 630. Location/Qualifiers	oy da	1186 AAATGTAAAGAAATGAATGCTGATGCGTGTTTGCATTCCAGTTGCGCAATCCTGTCCAC 1245 
source	1915 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Inagg:6374672"	QY	1246 AATGGCCATGCCCTGTTGATGCAGGACACCTGCCGCAGGCTCCTAGAGAGGGCTACAAG 1305 
	/tissue_type="lang" cell carcinoma" /issue_type="lang" cell carcinoma" /lab_host="DH10B (phage-resistant)" /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:	δγ	1306 CACCCGGT-CCTCCTACTACACCCTCTGGGCGGCTGG-ACCAAGGATGACGATGGCCTC 1363
	ECORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and	da .	1364 TAGACTGGGGGA 1375 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 860)
I (context: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Context: Robert Strawed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11429 row: c column: 23
High quality sequence stop: 851.
                                                                                                                                                                                                                                                                                                                                                                                    942 CAAGTTTGTCCTGGCACATGGTGGACGGAGGGTAGCTATCTTACGAGACGCTGAATTCTA 1001
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721. TGAACACAGAAAAGAAGAACGCTGTTCCCGTGTTTGGGGGAACACATGTACAAAACACC 780
                                                              421 GACCACGTCCGAGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTC
                                                                                                                                                  1002 TGAACACAGAAAAGAGGAACGCTGTTCCCGTGTTTGGGGGACAACATGTACAAAACACCC
                                            GACCACGTCCGAGCTGAGGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTC
                                                                                                                              CAGTGGGTCCAGGTTTTGAGCGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAG
                                                                                                                                                                                                                823 AAGGAGTACTACAGGTTATGCACTTTGACACCCTGCTAGATGATGGCGTGATCAACATG
                                                                                                                                                                                                                                                                                               883 AGCATCCCCATTGTACTGCCCGTCTCTGCAGAGATAAGACACG-GCTGGAAGGGTGCAG
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Homo sapiens
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                                                           BQ220909 872 bp mRNA linear EST 02-MAY-2002 AGENCOURT_7504327 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6049802
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/lab_host="DH10B (phage-resistant)"
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTCTGCATTACCAGCTTTATTTCTCCATTCGCAAAGGATCGTGAGAATGCCCGCAAA 402
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                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1301 row: a column: 03
High quality sequence stop: 645.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 2.8e-217;
0; Mismatches 21;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_72"
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179 c
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Similarity 97.3%;
0; Conservative (
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/clone_line_ring
//clone_line_ring
//tissue_type="large_cell carcinoma"
/ibshoat="bH10B (phage-resistant).
/note="Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAGG, Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTCCAGGTTTTGAGCGAAGGCTGGGCCACTCCCCTCAAAGGTTTCATGCGGGAGAAGG 826
 AGENCOURT_8795627 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6429903
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                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 949)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1990)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MC clone distribution information can lead is through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2618 row: n column: 16
High quality sequence stop: 587.
Location/Qualifiers
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Pred. No. 3e-207;
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/db_xref="taxon:9606"
/clone="IMAGE:6429903"
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ilarity 98.4%;
Conservative
     5', mRNA sequence.
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Pred. No. 2.8e-211;
0; Mismatches 28;
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586 120 646 180 206 240 991

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(Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library." BASE COUNT 269 a 242 c 284 g 246 t ORIGIN	Query Match 39.8%; Score 734.8; DB 13; Length 1041; Best Local Similarity 93.1%; Pred. No. 1.2e-204; Matches 858; Conservative 0; Mismatches 52; Indels 12; Gaps 8;	OY 1 ATGTCGGGGTCAAGAAGCAAAAGACGGAGAACCAGCAGAATCCACCAATGTAGTCTAT 60	OY         61         CAGGCCCACCATGTGAQCAGGAATAAGAGGGCAAGTGGTTGGAACAAGGGGTGGGTTC         120           11	Oy 121 CGAGGATGTACCGTGTGGCTAACAGGTCTCTCGGTGCTGGAAAAACAACGATTTT 180		Qy 241 GTCCGTCATGGCCTTAACAGAAATCTCGGATTCTCTCTCGGGGACAGAGAGAAAATATC 300	Oy 301 CGCCGGATTGCTGAGGTGGCTAAGCTGTTTGCTGATGCTGGTCTGGTCTGCATTACCAGC.360	QY         361 TTTATTTCTCCATTCGCAAAGGATCGTGAGAATGCCCGCAAAATACATGAATGA	Qy 421 CTGCCATTCTTGAAA-TATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGGCGT 479	Qy 480 AAAAGGCCTCTATAAAAGGGCCAGAGCTGGGGAATTAAAGGATTTACAGTATTGATTC 539	Oy 540 TGATTATGAGAAACCTGAAACTCCTGAGCGTGTGCTTAAAACCAATTTGTCCACAGTGAG 599	QY         600 TGACTGTGTCCACCAGGTAGTGGAACTTC-TGCAAGACCAGAACATTGTACCTATACTA         658	Qy 659 TAATC-AAAGATATCCACGAACTCTTTGTGCCGGAAAACAAACTTGACCACGTCCGAGCT 717	OY 718 GAGGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGG 775	OY 776 TTTTGAGGGAGGGTGGGCCACTC-CCCTCAAAGGTTTCATGCGGGGAGAAGGATA 830	QY 831 CTTACAGGTTATGCACTTTGACACCCTGCT-AGATGATGGCGTGA-TCAACATGAGCATC 888	Oy 889 CCCATGTACTGCCCGTCTCTG 910 
361 AGTACTTACAGGTTATGCACTTTGACACCCTGCTAGATGATGGCGTGATCAACATGAGCA 887 TCCCCATTGTACTGCCGTCTCTGCAGAGGATAAGACACGGCTGGAAGGGTGCAGCAAGT	DD 421 TCCCCATTGTACTGCCCGTCTCTGCAGGGTAAGACACGGCTGGAAGGGTCAGGAAGT 480 QY 947 TTGTCCTGGCACCATGGTGGACGGAGGGTATCTTACGAGCGCTGAATTCTATGAAC 1006 Db 481 TTGTCTGCAACCATGACGAACGGAAGAATTCTAATGAATTCTATGAATTCTATGAAC 1006 Db 481 TTGTCTTGCAACAATCAACAACAAAATTAAAAAAAA 540	1007 ACAGAAAGGAACGCTGTTCCCGTGTTGGGGGACAACATGTACAAAACAACCCCCATA 111111111111111111111	1067 TCAAAATGGTGAAGGGGACTGGCTGGTTGGTGGAGCACCCCCAIA 1067 TCAAAATGGTGAAAGTGGGGACTGGCTGGTTGGTGGAGACCTTCAGGTGCTGGAGA 601 TCAAAATGGTGAAGAGAGGGAATTGGGAATTGGTAGAAATTGGTAGAAATTGGGAAATTGGGAAATTGGGAAATTGGTAGAAAATGGTAAAGAAATTGGGAAATTGGGAAATTGGGAAATTGGGAAATTGGGAAATTGGTAAAGAAATTGGGAAATTGGGAAATTGGGAAATTGGGAAATTGGGAAAATTGGGAAAATTGGGAAATTGGTAAAATTGGAAAATTGGAAAATTGGAAAATTGGAAAATTGGAAAATTGGAAAATTGAAAGAAATTGGAAAATTGAAAGAAATTGGAAAATTGAAAGAAATTGAAAAATTGAAAAATTGAAAATTGAAAATTGAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAATTGAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAAA	1127 AAATAAGATGAATGATGGGCTGGACCAATACCGTCTGACACTCTGGAGCTCAAACAGA 661 AAATAAGATGGAATGATGGGCTGGACCAATACCGTCTGACACTCTGGAGCTCAAACAGA	1187 ANTGTAAAGAAAT-GAATGCTGATGCGGTG-TTTGCATTCCAGTTGCGCAATCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCC-TGTCCTGTTTTGCTTTCCAGTTTGCCAATCGCAATCGTTGTCCTGTCTTTGCTTTTCCAGTTTGCCAATCGTGTTGTCCTTGTCCTTGTCCTTGTCTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTTT		6	BIB29344 LOCUS LOCUS DEFINITION 603079477F1 NIH_MCC_119 Homo sapiens CDNA clone IMAGE:5171058 5', mRNA sequence.	ACCESSION BIR29344 VERSION BIR29344.1 GI:15940894 KEYWORDS EST. SOURCE human.	NOTATION ADDITION SETTINGS (CATAINATA: Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE I (bases I to 1041)	ADJUNCAS NATIONAL INCEPTION (MGC. DC. 1.111.1.90v/ TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D.	Tissue Procurement: Life Technologies, Inc.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Arrayed by: The I.M.G.E. Consortium (LLNL)	Days agenerally by: Incyle Genomics, inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Plate: LLAM11425 row: j column: 19 High quality sequence stop: 841. FEATURES Location/Qualifiers Source 1. 1041	/organism="Homo sapiens" /db_xref="taxon:9060" /clone="IMAGE:5171058" /clone_lib="XIH_MGC_119"	/lab_host="DH10B" /lab_host="DH10B" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from	anonymous male age 2/. Library is Oligo-df primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

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TGGCACATGGTGGACGGAGGG-----TAGCTATCTTACGAGACGCTGAATTCTAT-GAAC 1006
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5/ mRNA sequence.
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    599 GTGACTGTGTCCACCAGGTAGTGGAACTTCTGCAAGAGCAGAACATTGTACCTATACTA
                                                                                                                                                           AGGCTGAAACTCTCCCTTCATTATCAATTACTAAGCTGGATCTCCAGTGGGTCCAGGTTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2544 row: b column: 14
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High quality sequence stop: 688.
Location/Qualifiers
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/db_xref="taxon:9606"
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Mammalia; Eutheria;
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                               1054 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8836984 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6429378
5', mRNA sequence.
BQ942867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="repidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung, Vector: poTB7; Site_1: EcoRI; Site_2:
Xhoi: cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xhoi sites using the following 5' adaptor:
GCACGAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
131 c 279. g 254 t 5 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1054)
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2617 row: h column: 19
High quality sequence start: 24
High quality sequence stop: 736.
Location/Qualifiers
I. 1054
                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Artz
CDNA Library Preparation: Rubin Laboratory
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/clone_lib="NIH_MGC_101"
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                                                                                                                                  BQ942867.1 GI:22358345
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Corgan: lung: Vector: poTP8; site_1: XhoI; Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCACGAG(GG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SUBPERCIPTED II RT (Life Technologies). Note: this is a
127 c 244 g 193 t
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                                                                                                                                  Score 704.8; DB 14; Length 874;
Pred. No. 7.5e-196;
0; Mismatches 12; Indels 19;
                                                                                                                                   38.2%;
96.1%;
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Matches 761;
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="INAGE:6372309"
/clone="INAGE:6372309"
/clone=type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/tasue_type="large cell ca
      bp mRNA linear EST 21-AUG-2000
Homo sapiens cDNA clone IMAGE:6372309
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGTCGGGGATCAAGAAGAAGACGGAGAACCAGCAGAAATCCACCAATGTAGTCTAT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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225 c 252 g
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                                                                                                                                        5′, mRNA sequence.
BO935947
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601474242F1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3877186 5', mRNA sequence.
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and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                            Indels
                                                                                       Score 629; DB 12;
Pred. No. 1.4e-173;
0; Mismatches 5;
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BE786139.1 GI:10207337
                                                                                       Query Match 34.1%;
Best Local Similarity 98.5%;
Matches 677; Conservative
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TITLE
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/lab_host="DHIOB (T1 phage-resistant)"
/lab_host="DHIOB (T1 phage-resistant)"
/lab_host="DHIOB (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
S-ATTCTAGAGGCGGCGACATG-4T(30)BN-3' (Where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG484421 683 bp mRNA linear EST 21-MAR-2001 602505063F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618575 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                  CTGCCATTCTTTGAAATATTTGTAGATGCACCTCTAAATATTTGTGAAAGCAGAGGACGTA
                                                                                                                                                                                 AAAGGCCTCTATAAAAGGGCCAGAGCTGGGGAGATTAAAAGGATTTACAGGTATTGATTCT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMl376 row: n column: 16
High quality sequence stop: 674.
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Contact: Robert Strausberg, Ph.D.
Contact: Gapbs: r@mall.nlh.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
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/db_xref="taxon:9606"
/clone="IMAGE:4618575"
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BG484421
BG484421.1 GI:13416700
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                                  Email: cgapbs-remail.nh.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9639 row: c column: 11
High quality sequence stop: 648.
Location/Qualifiers
i. 650
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:187186"
/clone=lib="MHLMGC.68"
/tissue_type="large cell carcinoma"
/tab_host="Inage" lung: very resistent"
/note="Inage" lung: very report resistent"
/note="Inage" lung: very report repor
                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies.
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Pred. No. 2.3e-172;
); Mismatches 2; Indels 2;
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                      Contact: Robert Strausberg, Ph.D.
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p mRNA linear EST 26-JUN-2001
musculus cDNA clone IMAGE:5044119
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (Tl phage-resistant)"
/note="Vorgan: kidney; Vector: pcMv-SPORT6; Site_l: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. |"
195 c 222 g 177 t l others
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601 AATGATGGGCTGGACCAATA-CGTCTGACA-CTCTGGAGCTCAAACAGAAAT
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Pred. No. 4.3e-172;
0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                         BI103516 797 bp 602889057F1 NCI_CGAP_Kid14 Mus
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al Similarity 87.2%;
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BI103516
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AGGTCCAGTGGCACTGCAGGTCCCGGATGATTGCGGGGTGCCAATTTCTACATTGTGGGGGA 1534
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1295 GGGGCTACAAGCACCCGGTCCTCCTACTACACCCTCTGGGCGGCTGGACCAAGGATGACG 1354
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Custil Mark to State Shift